

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 10:09:13 ; Search time 6821 Seconds
(without alignments)
9941.290 Million cell updates/sec

Title: US-09-888-035A-1

Perfect score: 2330

Sequence: 1 gagaagagagttttagcg.....ttgaaaaaaaaaaaaaa 2330

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
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- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2313	99.3	2313	8	AB021878	AB021878 Oryza sat
2	828.8	35.6	2017	8	AY040245	AY040245 Triticum
3	793.4	34.1	2423	6	BD012814	BD012814 Gene codi
4	793.4	34.1	2423	8	AB051817	AB051817 Petunia x
5	793.4	34.1	2423	23	BD008249	BD008249 Gene codi
6	791.4	34.0	1668	6	E63046	E63046 Na+/H+ anti
7	791.4	34.0	1668	6	E63047	E63047 Na+/H+ anti
8	791.4	34.0	2637	6	AB038492	AB038492 Atriplex
9	790	33.9	2553	6	BD012815	BD012815 Gene codi
10	790	33.9	2553	8	AB051818	AB051818 Nierember
11	790	33.9	2553	23	BD008250	BD008250 Gene codi
12	777.6	33.4	2173	8	AB054979	AB054979 Ipomoea t
13	775	33.3	2135	8	AY028416	AY028416 Citrus x
14	768.8	33.0	1614	8	AF106324	AF106324 Arabidops
15	768.8	33.0	1617	8	AF510074	AF510074 Arabidops
16	768.8	33.0	1619	8	AF056190	AF056190 Arabidops
17	768.8	33.0	2218	8	AB033989	AB033989 Ipomoea n
18	768.8	33.0	2237	6	BD012802	BD012802 Gene codi
19	768.8	33.0	2237	23	BD008237	BD008237 Gene codi
20	766.8	32.9	1641	8	AF490586	AF490586 Arabidops
21	740.6	31.8	2263	8	AF370358	AF370358 Suaeda ma
22	727.8	31.2	126315	8	AP004274	AP004274 Oryza sat
23	712.4	30.6	2122	8	LES306630	LES306630 Lycopersi
24	711.8	30.5	2361	6	BD012816	BD012816 Gene codi
25	711.8	30.5	2361	8	AB051819	AB051819 Torenia h
26	711.8	30.5	2361	23	BD008251	BD008251 Gene codi
27	691.4	29.7	1693	8	AY040246	AY040246 Triticum
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29	470.6	20.2	1677	6	AX459657	AX459657 Sequence
30	361.4	15.5	612	8	AF515632	AF515632 Gossypium
31	245.4	10.5	320	8	AF307944	AF307944 Zea mays
32	239.2	10.3	421	8	AF279671	AF279671 Mesembrya
33	202	8.7	459	8	AF279670	AF279670 Mesembrya
34	124.2	5.3	90019	8	TM021804	TM021804 Arabidops
35	119.4	5.1	116416	2	AC130801	AC130801 Medicago
36	108	4.6	93234	8	AC009465	AC009465 Arabidops
37	107	4.6	86022	8	ATAC011623	ATAC011623 Arabidops
38	101.6	4.4	139627	2	AC016779	AC016779 Oryza sat
39	97	4.2	567	11	AL772701	AL772701 Arabidops
40	96.4	4.1	2401	3	AF497828	AF497828 Caenorhab
41	96.4	4.1	2453	3	AF497829	AF497829 Caenorhab
42	96.4	4.1	7545	8	AB033990	AB033990 Ipomoea n
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44	94	4.0	132693	2	AP003543	AP003543 Oryza sat
45	94	4.0	149040	2	AP003507	AP003507 Oryza sat

ALIGNMENTS

RESULT 1

AB021878

LOCUS AB021878

DEFINITION Oryza sativa (japonica cultivar-group) OsnHX1 mRNA, complete cds.

ACCESSION AB021878

VERSION AB021878.1 GI:5731736

KEYWORDS Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) cDNA to mRNA.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1

AUTHORS Fukuda,A., Nakamura,A. and Tanaka,Y.

TITLE Molecular cloning and expression of the Na⁺/H⁺ exchanger gene in
 JOURNAL Biochim. Biophys. Acta 1446 (1-2), 149-155 (1999)
 MEDLINE 99326147
 REFERENCE 2 (bases 1 to 2313)
 AUTHORS Fukuda, A., Tanaka, Y. and Nakamura, A.
 TITLE Direct Submission
 JOURNAL Submitted (25-DEC-1998) Atsunori Fukuda, National Institute of
 Agrobiological Resources, Department of Plant Physiology, Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail: fukuda@abr.affrc.go.jp, Tel: 81-298-38-8376,
 Fax: 81-298-38-8347)

FEATURES

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 1..2313
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BASE COUNT 543 a 538 c 569 g 663 t

Query Match 99.3%; Score 2313; DB 8; Length 2313;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	TCTCGAATCGAATCTTGTGTTTCTTCTAATTTTACGGGAATGCGAATAGG	180
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RESULT 2
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DEFINITION Triticum aestivum Na+/H+ antiporter (NHX1) mRNA, complete cds.
ACCESSION AY040245
VERSION AY040245.1 GI:15027832
KEYWORDS Triticum aestivum.
SOURCE Triticum aestivum.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticeae; Triticeae; Triticeum.
1 (bases 1 to 2017)
REFERENCE Wang, Z., Zhang, J. and Chen, S.
AUTHORS Isolation and characterization of two Na+/H+ antiport genes from
TITLE wheat
JOURNAL Unpublished

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2 (bases 1 to 2017)
Wang, Z., Zhang, J. and Chen, S.
Direct Submission
Submitted (14-JUN-2001) Institute of Genetics, Chinese Academy of
Sciences, Dacun Road 3, Beijing 100101, China
Location/Qualifiers
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Qy	1600	TGATGACAAGCCATTTGATCAGGCTGCTCTACCGGCTCAGGCCATCTGTCACCTCTG	1659
Db	1464	TGCTGACTAAGCCTCTGATTATCTCTCTCATCCCAACGA-----CTTGGCACCGCAG	1517
Qy	1660	AGCCTTCAATCAACAAAGTCCCTGCAATTCCTCTCTGACAAGCATGCAAGTTCTTGACC	1719
Db	1518	CTGATATCTCAAGCCAGTCAATTCCTAGACCCACTTACGGCGAGCTTGTGGGGTCGACT	1577
Qy	1720	TCGAGAGTACAACCAACATTGTGAGGCCTTCCAGCCTCCGATGCTCTCTCACCAAGCCGA	1779
Db	1578	TCGA---TGTAGGCGAGCTCACCCCCAAAACAACCTTTCAATTTCTCACCATGCGCAA	1634
Qy	1780	CCCACTGTCCACTACTCTGGCGCAAGTTTCGACGACGCGCTCATCGCACCATGTTTG	1839
Db	1635	CTCGCTCGGTTTATCGTGTATGCGCAAGTTTCGATGATAGTTTCATGCGGCCAATGTTTG	1694
Qy	1840	GCGGGCGCGGTTTCGTGCCCTTCTCCCTTGGATCAACCAACGACGAGC	1889
Db	1695	GGGGAAGAGGCTTCGTCCATTTGTGCTGTGTTCACTGCTTCACTAGAGGAGC	1744

RESULT 3				
BD012814				
LOCUS				
DEFINITION	BD012814	2423 bp	DNA	linear PAT 02-AUG-2002
	Gene coding for protein having an activity to control pH in vacuoles.			
ACCESSION	BD012814			
VERSION	BD012814.1	GI:22093003		

KEYWORDS	WO 0114560-A/13.
SOURCE	Petunia x hybrida.
ORGANISM	Petunia x hybrida
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
REFERENCE	1 (bases 1 to 2423)
AUTHORS	Iida,S., Tanaka,S. and Inagaki,Y.
TITLE	Gene coding for protein having an activity to control pH in vacuoles
JOURNAL	PATENT: WO 0114560-A 13 01-MAR-2001.
COMMENT	SUNTORY LTD,SHIGERU IIDA,SACHIKO TANAKA,YOSHISHIGE INAGAKI OS Petunia hybrida
	PN WO 0114560-A/13
	PD WO 0114560-A/13
	PF 24-AUG-2000 WO 2000JP005722
	PR 24-AUG-1999 JP 99P 236800
	PI SHIGERU IIDA,SACHIKO TANAKA,YOSHISHIGE INAGAKI PC C12N15/29,C07K14/415,C12N5/10,A01H5/00,C12P21/02 CC Nucleotide sequence of DNA coding for protein having an activity to
	CC control pH in vacuoles
FEATURES	Source
	Feature Key Location/Qualifiers.
	1..2423
	/organism="Petunia x hybrida"
	/db_xref="taxon:4102"
BASE COUNT	621 a 428 c 518 g 856 t
ORIGIN	
	Query Match 34.1%; Score 793.4; DB 6; Length 2423;
	Best Local Similarity 69.9%; Pred. No. 1.8e-164;
	Matches 1089; Conservative 0; Mismatches 461; Indels 9; Gaps 1;
Qy	335 GTACACGACCTCGACTACCGGTCGGGFGTGCATCAACCTGTTGGTCGCGTCTGTG 394
Db	393 GTTATCGACATCTGATCATCAATCAGTGTGTGCGATAAACTTATCGTGTCTTATTG 452
Qy	395 CGCTCGCATCGTCTCGGCCACCTCCTCGAGGAGATCGGTGGTCAATGAGTCCATCAC 454
Db	453 CGCGTGATTGTGATCGGTCAATTGTGGAGAAGAACAGATGATGAATGAGTCCATAAC 512
Qy	455 CGCGCTCATCATCGGGCTCTGCACCGCGTGGTGATCTTGTCTGATGACCAAGGGAAGAG 514
Db	513 TGCCTTAGTCATTTGGTTCTTGTACTCGAATCGTTATTTCTACTGTAAGTGGAGAAAGAA 572
Qy	515 CTGCACTTATTCGTCTTCAGTCAGATCTCTTCTTCATCTACTCCTCCTCCGATCAT 574
Db	573 CTCTCATATTTTAGTGTTCAGTGAAGATCTTTTCTTCATTTACTTTCCTCCGCAATCAT 632
Qy	575 CTTCAATGCAAGTTTTCAGGTAAAGAAAAGCAATTTCTCCGGAATTTTCATGACGATCAC 634
Db	633 TTTTAAATGCTGGGTTCCAGGTGAAAAGAAATCGTTTCTTCGCAATTCAGCACATCAT 692
Qy	635 ATTATTTGGAGCGTCGGGCAATGATATCTTTTTCACAAATCATTTAGTGTGCCATTGC 694
Db	693 GCTCTTTGGGGCACTTTGGCACCTTGATATCATTCATTTATATATCATTTAGTGTCCATTGG 752
Qy	695 AATATTTCAGCAGAAATGAACATTGGAAAGCGTGGAGTGTAGGAGATTTTCTTGGCAATTTGGAGC 754
Db	753 CATTTTCAAGAAATGAATATTGGAAAGCCTTGAATTTGGAGATTACCTTTGCAATTTGGGGC 812
Qy	755 CATCTTTTTCGACAGATTTCTGTCTGCATATTCGAGGTCTCTCAATTCAGGATGAGACCC 814
Db	813 AATCTTCTCTGTACAGATTTCTGTATGCACTTGTATGCACTTACAAAGTCTTAATCAGGATGAACACC 872
Qy	815 CTTTTTTGTACAGTCTGSTATTCGGTCAAGGTGTGTGAACGATGCTACATCAATTTGTGCT 874
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Qy	875 TTTCAACGCACTACAGAACTTTGATCTTCTGCACATAGATGCGGCTGTCTGAAAT 934
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Qy 815 CTTTTTGTACAGTCTGGTATTTCTGGTGAAGGTGTTGTGAACGATGCTACATCAATTTGTGCT 874
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Qy 1115 CGGCACTTCCACCGTATTTCTTGTGGTATTTGTAATGTCATATACACTTGGGCAATACGT 1174
Db 1173 TGCATCTCACTGTTTTCTCTGGATCGTATGCTTACCTTACCTGCTGCGCATATATGT 1232
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Qy 1235 GACTTTTCTTCTCTGATGTTGGATGCGATGCGATTTGAAATTTGAAATTTGGAGTTTGC 1294
Db 1293 AATATTCTATTTCTTTATTTGTTGATGATGCTTTGACATTTGAGAATTTGGAATTTGT 1352
Qy 1295 CAGTCACAGACCTGGCAATCCATTTGGGATAAGCTCAATTTTGTAGGATTTGTTCTGAT 1354
Db 1353 AAGCAGACAGCCCTGGAATATCAGTTTCAGTTAGCTTCAATATTTGCTGGTCTTTGTTGGT 1412
Qy 1355 TGGAAAGAGCTGTTTGTATTTCCCGCTCTGCTTCTTGTGCAACCTTAACAAAGAGGCAACC 1414
Db 1413 TGGAAAGAGCAGATTTGTTTCCCATTTGTCATTTCTGTGCACTTACCAAGAAATCTCC 1472
Qy 1415 GAATGAAAAATAAATCTGGAGACAGCAAGTTGTATATTTGTTGGCTGGGCTGGCTGATGAGG 1474
Db 1473 AGAGGCGAAAAATAGTTTAAACAGCAGGTTTACAATATTTGTTGGCTGGACTTATGAGAGG 1532
Qy 1475 AGCTGTGTCGATTTGCTTGTCTTCAATAAGTTTACAGATCTGGCCATCTACAGTGTCA 1534
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Db 1713 AATGATCTCTTCTGAACCAAGACCCCAAAATCTTCAATGTGCGACCTTTTGACAGCAC 1772
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Qy 1826 GCGACCGATGTTTGGCGGCGGGTTCGTGCGCTTCTCCCTGTGATCACCAACCGAGC 1884
Db 1893 GCGTCCAGTTTTCGGTGGACGAGGTTTGTACCTTTTGTCTCCAGGATCACCGACAGAC 1951

RESULT 6
E63046 1668 bp DNA linear PAT 31-JAN-2002
LOCUS Na+/H+ antiporter protein and gene encoding it.
DEFINITION E63046
ACCESSION E63046
VERSION E63046.1 GI:18628471
KEYWORDS JP 2000157287-A/1.
SOURCE unidentifed.
ORGANISM unidentifed.
REFERENCE 1 (bases 1 to 1668)
AUTHORS Shono,M., Hayakawa,T. and Tanaka,A.
TITLE Na+/H+ antiporter protein and gene encoding it
JOURNAL Patent: JP 2000157287-A 1 13-JUN-2000;
PLANTECH RESEARCH INSTITUTE
COMMENT OS Atliplex Gmelini
PN JP 2000157287-A/1
PD 13-JUN-2000
PF 16-SEP-1999 JP 1999261606
PR
PI MARIKO SHONO, TAKAHIKO HAYAKAWA, AKIRA TANAKA
PC C12N15/09, A01H5/00, C07K14/415, C12Q1/68//C12N5/10, C12N15/00, PC
C12N5/00
CC

PH Key Location/Qualifiers
FT source 1..1668
FT /organism='Atliplex gmelini'.
FEATURES
source 1..1668
/organism='unidentifed'
/db_xref='taxon:32644'
BASE COUNT 397 a 342 c 376 g 553 t
ORIGIN

Query Match 34.0%; Score 791.4; DB 6; Length 1668;
Best Local Similarity 70.0%; Pred. No. 4.8e-164;
Matches 1115; Conservative 0; Mismatches 436; Indels 42; Gaps 2;

Qy 339 ACAGACCTCGACCTACCGCTCGGTGTGTCATCAACCTGTCGTGCGCTGCTGTCGCGC 398
Db 49 ACCACTTGTATCACGCTTCTGTGCTCGATGAACCTGTTGTGGCACTGTTATGTGT 108
Qy 399 TGCATCGTCTCTCGGCCACCTCTCGAGGAGAAATCGCTGGGTCAATGAGTCCATCACCG 458
Db 109 TGTATCGTAATTTGGTTCATCTTCTAGAGGAGAAATCGTTGGATGAATGAGTCCATCTGC 168
Qy 459 CTATCATCTGGGCTTGCACCGCGCTGCTGCTGATGACCAAGGAGAGACTCG 518
Db 169 CTTCTTATAGTTTGGCTACTCGGGTGTGATTTCTGCTGATTTAGTGGAGGAAAAAGTTCA 228
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QY 759 TTTTCTGACACAGATTCTCTGTCGACATTCAGAGTCTCAATCAGATGAGACACCCCTTT 818
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QY 1059 CTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCTGAGTTGCTAGATTTGAGCGGC 1118
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QY 1299 GACAGACTTGGCAATTCATTTGGGATAAGCTCAATTTTGTAGGATTTGTTCTGATTTGA 1358
Db 1009 GATAGTCTCGGCATTTCTGTTGCTGTGAGTTCCATATTTGCTAGTCTAGTCAATGTTGA 1068
QY 1359 AGAGCTGCTTTGTATTTCCGCTGTCTGTTTGTGCAACCTTAACAAGAGGCAACCGAAT 1418
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QY 1419 GAAAAATAAACCCTGAGACAGCACTTTGTAATATGTTGGCTGGCTGATGAGAGACT 1478
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Db 1609 CCTTTGTCCCGGGTTCACTTACTGAACAAGC 1641

RESULT 7
E63047 Na+/H+ antiporter protein and gene encoding it. linear PAT 31-JAN-2002
LOCUS E63047
DEFINITION E63047
ACCESSION E63047
VERSION E63047.1 GI:18628472
KEYWORDS JP 2000157287-A/2.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1668)
AUTHORS Shono,M., Hayakawa,T. and Tanaka,A.
TITLE Na+/H+ antiporter protein and gene encoding it
JOURNAL Patent: JP 2000157287-A 2 13-JUN-2000;
COMMENT PLANTECH RESEARCH INSTITUTE
OS Atliplex gmelini
PN JP 2000157287-A/2
PD 13-JUN-2000
PF 16-SEP-1999 JP 1999261606
PR
PI MARIKO SHONO,TAKAHIKO HAYAKAWA,AKIRA TANAKA
PC C12N15/09,A01H5/00,C07K14/415,C12Q1/68//C12N5/10,C12N15/00, PC
C12N5/00
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FEATURES
source Location/Qualifiers
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BASE COUNT 397 a 342 c 376 g 553 t
ORIGIN
Query Match 34.0%; Score 791.4; DB 6; Length 1668;
Best Local Similarity 70.0%; Pred. No. 4.8e-164;
Matches 1115; Conservative 0; Mismatches 436; Indels 42; Gaps 2;
QY 339 ACGACCTCCGACTACGGCTCGGTGTGTCATCAACCTGTTCTGTCGCGCTGCTCTGCGCC 398
Db 49 ACCACTTCTGATCAGCTTCTGCTGCTCGATGAATTTGTTGGCACTGTTATGTGT 108
QY 399 TGCATGCTCTCGGCCACCTCTCAGGAGAAATCGTGGGTCAATGAGTCATCAACCGG 458
Db 109 TGTATCTAAATGCTGATCTTCTAGAGGAAATCGTTGGATGAATGATCCATCACTGCC 168
QY 459 CTCTATCATCGGGCTCTGCACCGGCTGTGATCTTGTGTGATGACCAAGGAAAGAGCTCG 518
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QY 519 CACTTATTCGTTTCAGTGAGGATCTCTTCTTCATCTACCTCTCCCTCCGATCATCTTC 578
Db 229 CATCTTTTGGTCTTTCAGTGAAGATCTTTTCTTCATATACCTCTTCCACCGATTATATTC 288
QY 579 AATCAGGTTTTCAGGTAAAGAAAGCAATTTCTCCGGAATTTTCATCAGCATCACATTA 638
Db 289 AATCAGGCTTTTCAGGTGAAGAAAGCAATTTCTCCGCAACTTCTTCACTTATTTGTTAT 348
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Best Local Similarity 70.0%; Pred. No. 4.9e-164;
Matches 1115; Conservative 0; Mismatches 436; Indels 42; Gaps 2;

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QY 339 ACAGCTCGACTAGCGTGGTGGTCCATCAACCTCTTGGTGGCGTGTCTGGCC 398
Db 730 ACCACTTCTGATACACGCTTCTGGTGGTCTGATGAACCTTGTGGTGGTGGT 789
QY 399 TGCATGCTCTCGGCGACCTCTCCAGAGAGAAATCGCTGGGTCAATGAGTCCATCACCGG 458
Db 790 TGTATCGTAATTTGGTCACTCTCTAGAGGAGAAATCGTGGTGAATGAGTCCATCACTGCC 849
QY 459 CTCATCATCGGCTCTGCAACCGCGTGGTGAATCTGCTGATGACCAAGGAGAGCTCG 518
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Db 1750 AGAGCAGCTTTTGTGTTTCCCTTATCTCTGTTGATGAACCTTTGCCAAGAAATCGAAAGT 1809
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Db 1810 GAAAGGTCATTTTCAACACAGAGATTTGCATATGTTGGCTGGTCTTATGAGAGTGTCT 1869
QY 1479 GTGTCGATTTGCTTCTTCTTACAAATTAAGTTTACAGATCTGGCCATCTCAGCTGCACGCG 1538
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Db 2290 CTTTGTGTCGGGTTTCACTTACTGAAACAAAGC 2322
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RESULT 9
LOCUS BD012815 2553 bp DNA linear PAT 02-AUG-2002
DEFINITION Gene coding for protein having an activity to control pH in vacuoles.

ACCESSION BD012815
VERSION BD012815.1 GI:220933004

KEYWORDS WO 0114560-A/14.

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2553)

AUTHORS Iida S., Tanaka, S. and Inagaki, Y.

TITLE Gene coding for protein having an activity to control pH in vacuoles

JOURNAL Patent: WO 0114560-A 14 01-MAR-2001;

COMMENT SENTRY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI

OS Nierembergia hybrida

PN WO 0114560-A/14

PD 01-MAR-2001

PF 24-AUG-2000 WO 2000JP005722

PI 24-AUG-1999 JP 99P 236800

CC C12N15/29, C07K14/415, C12N5/10, A01H5/00, C12P21/02 CC Nucleotide sequence of DNA coding for protein having an activity to

CC control pH in vacuoles

PH Key Location/Qualifiers.

Source 1. .2553

/organism="unidentified"

/db xref="taxon:32644"

BASE COUNT 666 a -487 c 535 g 865 t

ORIGIN


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xx RN 1-2553
xx RA Iida S., Tanaka S., Inagaki Y.;
xx RL "Gene coding for protein having an activity to control pH in vacuoles";
xx RL Patent number JP03075543-T/14, 23-FEB-2001.
xx RL SUNTORY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI.
xx OS Nierembergia hybrida
xx CC PN JP 03075543-T/14
xx CC PD 23-FEB-2001
xx CC PF 24-AUG-2000 JP 2000005722
xx CC PR 24-AUG-1999 JP 99P 236800
xx CC PI SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI
xx CC PC C12N15/29, C07K14/415, C12N5/10, A01H5/00, C12P21/02
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Best Local Similarity 69.7%; Pred. No. 1e-163;
Matches 1088; Conservative 0; Mismatches 465; Indels 9; Gaps 1;

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QY 1890 CA 1891
DB 2136 GA 2137

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RESULT 12
AB054979
LOCUS
DEFINITION
ACCESSION

AB054979 2173 bp mRNA linear PLN 19-JUN-2001
Ipomoea tricolor ItNHX1 mRNA for Na+/H+ exchanger, complete cds.
AB054979

VERSION	AB054979.1	GI:14488269	
KEYWORDS	Ipomoea tricolor cDNA to mRNA.		
SOURCE	Ipomoea tricolor		
ORGANISM	Ipomoea tricolor		
REFERENCE	Ipomoea tricolor cDNA to mRNA.		
AUTHORS	Yamaguchi, T., Fukuda-Tanaka, S., Inagaki, Y., Saito, N., Yonekura-Sakakibara, K., Tanaka, Y., Kusumi, T. and Iida, S.		
TITLE	Genes encoding the vacuolar Na ⁺ /H ⁺ exchanger and flower coloration		
JOURNAL	Plant Cell Physiol. 42 (5), 451-461 (2001)		
MEDLINE	21276661		
REFERENCE	2 (bases 1 to 2173)		
AUTHORS	Fukuda-Tanaka, S., Inagaki, Y., Yamaguchi, T. and Iida, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JAN-2001) Sachiho Fukuda-Tanaka, National Institute for Basic Biology, Division of Gene Expression and Regulation 1; Myodaiji-cho, Okazaki, Aichi 444-8585, Japan (E-mail: sachiho@nibb.ac.jp, Tel: 81-564-55-7682, Fax: 81-564-55-7685)		
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RESULT 13
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DEFINITION Citrus x paradisi sodium/proton exchanger mRNA, complete cds.
ACCESSION AY028416
VERSION AY028416.2 GI:15812034
KEYWORDS Citrus x paradisi.
SOURCE Citrus x paradisi.
ORGANISM Citrus x paradisi.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 2135)
Porat,R., Povancello,D., Ben-Hayyim,G. and Lurie,S.
A heat treatment induced the expression of a Na+/H+ antiport gene
(cNHX1) in citrus fruit
Plant Sci. 162 (6), 957-963 (2002)
2 (bases 1 to 600)
Porat,R., Lurie,S. and Povancello,D.
Direct Submission
Submitted (05-MAR-2001) Postharvest Sciences, ARO, The Volcani
Center, Bet Dagan 50250, Israel
3 (bases 1 to 2135)
Porat,R., Lurie,S. and Povancello,D.
Direct Submission
Submitted (01-OCT-2001) Postharvest Sciences, ARO, The Volcani
Center, Bet Dagan 50250, Israel
Sequence update by submitter
On Oct 1, 2001 this sequence version replaced gi:13508486.
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Qy 1469 GAGGAGCTGTGTGCTGTTGCTTCTTGTCTTACAATAAGTTTACAAGATCTGGCCATCTCA 1528
Db |||||
1167 GAGAGTCTGTATCTATGCTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1226
Qy 1529 GCTGACCGGCAATGCAATAATGATCACAGCACCATCACTGTGCTTCTTTTGTAGCACTAT 1588
Db |||||
1227 TGTACCGCGGAATGCAATCATGATCACGAGTACGATACTGTCTGTCTTTTGTAGCACAGT 1286
Qy 1589 GGTATTTGGGATGATGACAAAGCCATTTGATCAGGCTGTGCTACCGGCTCAGGCCATCC 1648
Db |||||
1287 GGTGTTGGTATGTGACCAACCACTCATAGCTACCTATTTACCGCACAGAACGCCAC 1346
Qy 1649 TGTCACTCTCTGAGCTTCTCATCAAGTCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1702
Db |||||
1347 CACGAGCATGTTATCTGATGACACACCCCAAAATCCATACATATCCCTTTGTGGACCA 1406
Qy 1703 CATGCAAGGTTCTGACCTCGAGAGTACAAACCAATTTGTGAGGCTTCCAGCTCCGGAT 1762
Db |||||
1407 AGACTCGTTCAATTGAGCCTTCAGGGAACCAAAATGTGCTCGGCTGACAGTATACGTGG 1466
Qy 1763 GCTCTCACCAAGCGGACCCACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1822
Db |||||
1467 CTTCTTGACAGCGCCCATCTCGAACCGTGATTTACTTGGAGACAAATTTGATGACTCCTT 1526
Qy 1823 GATCGACCGGATTTTGGCGGCGGGGTTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1882
Db |||||
1527 CATGCGACCCGCTTTTGGAGTCTGGGCTTTGTACCCCTTTGTTCCAGGTTCTCCCACTGA 1586
Qy 1883 GCAGAGCCAT 1892
Db |||||
1587 GAGAAACCT 1596

Search completed: April 5, 2003, 14:52:29
Job time : 6834 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 10:03:13 ; Search time 541 Seconds
(without alignments)
9698.995 Million cell updates/sec

Title: US-09-888-035A-1
Perfect score: 2330
Sequence: 1 gagaagagaggtttgtgcg.....ttgaaaaaaaaaaaaaa 2330

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2330	100.0	2330	21	AAA61876
2	793.4	34.1	2423	22	AAF75764
3	791.4	34.0	1668	21	AAAF72926
4	790	33.9	2553	22	AAF75765
5	768.8	33.0	2178	20	AAZ22591
6	768.8	33.0	2237	22	AAF75752
7	746.8	32.1	2284	20	AAZ22595
8	711.8	30.5	2361	22	AAF75766
9	508.8	21.8	1788	20	AAZ22592

10	482.8	20.7	1674	24	ABK12638	DNA encoding Physc
11	340.4	14.6	378	20	AAZ22606	Rice Na/H antiporter
12	139.2	6.0	330	20	AAZ22611	Arabidopsis Na/H a
13	138.8	6.0	281	24	ABL73323	Corn tassal-derive
14	109.4	4.7	1824	21	AAC95372	Cat flea HMT Na/H
15	109.4	4.7	1824	21	AAC95373	Cat flea HMT Na/H
16	109.4	4.7	2080	21	AAC95370	Cat flea HMT Na/H
17	109.4	4.7	2080	21	AAC95371	Cat flea HMT Na/H
18	92.2	4.0	268	20	AAZ22607	Rice Na/H antiporter
19	91.6	3.9	2449	23	ABL05095	Drosophila melanog
20	89.4	3.8	3727	24	ABK83214	Human transporter
21	77	3.3	1683	20	AAZ22602	Arabidopsis thalia
22	66.8	2.9	1688	22	AAF97930	Human secreted pro
23	65.2	2.8	2407	24	AAZ27260	Human transporter
24	65	2.8	1581	22	AAF97895	Human secreted pro
25	64.2	2.8	2617	23	ABL17669	Drosophila melanog
26	64	2.7	5597	22	AAH98721	Human EST-derived
27	62.6	2.7	2584	18	AAZ51330	Human Na+/H+ excha
28	62.6	2.7	2584	23	AAZ22603	DNA encoding novel
29	59.8	2.6	7778	23	ABL17668	Drosophila melanog
30	58.4	2.5	4408	24	ABL61776	Colon adenocarcino
31	58.4	2.5	4598	24	ABK35727	cDNA sequence #118
32	52.4	2.2	1354	22	AAF97931	Human secreted pro
33	52.4	2.2	4794	23	AAZ94071	DNA encoding novel
34	51.8	2.2	1964	23	ABL03375	Drosophila melanog
35	51.4	2.2	2890	24	AAZ22593	Human transporter
36	47	2.0	714	20	AAZ22593	Arabidopsis thalia
37	47	2.0	2122	20	AAZ22603	Arabidopsis thalia
38	46.8	2.0	263	21	AAA44056	Human secreted exp
39	46.4	2.0	2753	22	AAZ22660	Human secreted pro
40	44.6	1.9	1536	23	AAZ575121	DNA encoding novel
41	44.6	1.9	3489	21	AAA30290	Kaposi's sarcoma-a
42	44.6	1.9	3489	22	AAF82901	Nucleotide sequenc
43	44.6	1.9	3489	24	ABA93487	Kaposi's sarcoma-a
44	44.6	1.9	32207	20	AAV73805	KSHV LUR DNA (nucl
45	44.6	1.9	137507	19	AAV19941	KSHV long unique c

ALIGNMENTS

RESULT 1

AAA61876
ID AAA61876 standard; cDNA; 2330 BP.

XX
AC AAA61876;

XX
DT 07-NOV-2000 (first entry)

XX
DE cDNA encoding rice Na+/H+ antiporter, OsNHX1.

XX
KW OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter;
active transport; rice; transgenic plant; salt-tolerance; ss.

XX
OS Oryza sativa.

XX
FH Key Location/Qualifiers

FT CDS 297..1904

FT /tag= a

FT /product= "Rice Na+/H+ antiporter"

PN WO200037644-A1.

XX
PD 29-JUN-2000.

XX
PF 22-DEC-1999; 99WO-JP07224.

XX
PR 22-DEC-1998; 98JP-0365604.

XX
PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.

XX
PI Fukuda A, Tanaka Y;

DR WPI; 2000-442672/38.
 DR P-PSDB; AAB11832.
 XX
 PT DNA encoding a sodium ion and proton counter-transporter protein of
 PT rice origin for production of salt tolerant rice transformants -
 XX
 PS Claim 1b; Fig 1; 43pp; Japanese.
 XX
 CC This sequence represents cDNA encoding a rice Na⁺/H⁺ antiporter
 CC (countertransporter), OsNHX1. The invention relates to OsNHX1 and
 CC nucleic acids which encode it; vectors, host cells and transgenic plants
 CC containing OsNHX1 nucleic acids; recombinant expression of OsNHX1; and
 CC antibodies which recognise OsNHX1. OsNHX1 nucleic acids are useful in the
 CC production of salt tolerant transgenic plants.
 XX
 SQ Sequence 2330 BP; 560 A; 538 C; 569 G; 663 T; 0 other;

Query March 100.0%; Score 2330; DB 21; Length 2330;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAAAGAGATTCTAGCGAGCTCGCGAATGCGAAGCCAAACGAGAGAGGTCTCGAT 60
 Db |||||
 Qy 1 GAGAAAGAGATTCTAGCGAGCTCGCGAATGCGAAGCCAAACGAGAGAGGTCTCGAT 60
 Db |||||
 Qy 61 ACCAAATCCCGATTCTCAACCTGAATCCCCCCCCACGTTCTCTGTTCAATCTGTTG 120
 Db |||||
 Qy 61 ACCAAATCCCGATTCTCAACCTGAATCCCCCCCCACGTTCTCTGTTCAATCTGTTG 120
 Db |||||
 Qy 121 TCTGGAAATCGAATCTTTGTTTCTTCTAATTTTACGGGAATGTCGAATTAGG 180
 Db |||||
 Qy 121 TCTGGAAATCGAATCTTTGTTTCTTCTAATTTTACGGGAATGTCGAATTAGG 180
 Db |||||
 Qy 181 CATTCAACCAACGAGAGAGGAGTGGATTGGTTTAAAGTCCCGCATCTTCGGCGC 240
 Db |||||
 Qy 181 CATTCAACCAACGAGAGAGGAGTGGATTGGTTTAAAGTCCCGCATCTTCGGCGC 240
 Db |||||
 Qy 241 GAAATCTCGCTCTCTCTCTCGGTGGGTGGCGGAGAGTGGCGCGGTGAGGCATGG 300
 Db |||||
 Qy 241 GAAATCTCGCTCTCTCTCTCGGTGGGTGGCGGAGAGTGGCGCGGTGAGGCATGG 300
 Db |||||
 Qy 301 GGATGGAGTGGCGGCGGCGGTGGCGGCTCTGTACAGACCTCCCGCATCGGTGG 360
 Db |||||
 Qy 301 GGATGGAGTGGCGGCGGCGGTGGCGGCTCTGTACAGACCTCCCGCATCGGTGG 360
 Db |||||
 Qy 361 TGGTGTCCATCAACCTGTTCTGCGGCTGCTCTGCGCTGATCGTCTCGGCCACCTCC 420
 Db |||||
 Qy 361 TGGTGTCCATCAACCTGTTCTGCGGCTGCTCTGCGCTGATCGTCTCGGCCACCTCC 420
 Db |||||
 Qy 421 TCGAGGAGAAATCGTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCACCG 480
 Db |||||
 Qy 421 TCGAGGAGAAATCGTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCACCG 480
 Db |||||
 Qy 481 CGGTGGTCACTCTGATGATGACCAAGGAGAGCTCGCATTTATTCGTCTCAGTGAGG 540
 Db |||||
 Qy 481 CGGTGGTCACTCTGATGATGACCAAGGAGAGCTCGCATTTATTCGTCTCAGTGAGG 540
 Db |||||
 Qy 541 ATCTCTTCTTCACTACCTCTCTCTCGCATCATCTTCAATGCAAGTCTTTCAGGTAAAGA 600
 Db |||||
 Qy 541 ATCTCTTCTTCACTACCTCTCTCTCGCATCATCTTCAATGCAAGTCTTTCAGGTAAAGA 600
 Db |||||
 Qy 601 AAAAGCAATCTTCGGGAATTTATGATGATGATGATGATGATGATGATGATGATGATG 660
 Db |||||
 Qy 601 AAAAGCAATCTTCGGGAATTTATGATGATGATGATGATGATGATGATGATGATGATG 660
 Db |||||
 Qy 661 TATCTTTTTCACATATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db |||||
 Qy 661 TATCTTTTTCACATATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db |||||
 Qy 721 CGCTGGATGATGAGGATTTTCTTGGAAATGGAGGCTCTTTCTGCGACAGATCTGTCT 780
 Db |||||
 Qy 721 CGCTGGATGATGAGGATTTTCTTGGAAATGGAGGCTCTTTTCTGCGACAGATCTGTCT 780
 Db |||||

Qy 781 GCACATTGCGAGTCTCTCAATCAGGATGAGACACCTTTTCTGATCAGTCTGTTATTCGGTG 840
 Db |||||
 Qy 781 GCACATTGCGAGTCTCTCAATCAGGATGAGACACCTTTTCTGATCAGTCTGTTATTCGGTG 840
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 Qy 841 AAGGTGTGTGAACGATGCTACATCAATTTGCTTTTCAACGCACTACAGAACTTTGATC 900
 Db |||||
 Qy 841 AAGGTGTGTGAACGATGCTACATCAATTTGCTTTTCAACGCACTACAGAACTTTGATC 900
 Db |||||
 Qy 901 TTGTCCACATAGATGCGGCTGCTGTTCTGAAATTTCTTGGGAACTTCTTTTATTTATTTT 960
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 Qy 901 TTGTCCACATAGATGCGGCTGCTGTTCTGAAATTTCTTGGGAACTTCTTTTATTTATTTT 960
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 Qy 961 TGTGAGACACCTTCTTGGAGTATTGCTGGAATGCTCAGTGCATACATAAATCAAGAAGC 1020
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 Qy 1021 TATACATTGAGGCAATCTTACTACCGTGAAGTGGCTTTATGATGCTCATGCTTACC 1080
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 Qy 1081 TTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCAATCTCACCGTATTTCTTCTGTG 1140
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 Qy 1141 GTATTGTAATGTCAATACATTGGAATACGTCACAGAGAGTTCAAGAGTTACAAAC 1200
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 Db |||||
 Qy 1261 TGGATGATTTGGAATTTGAAAAATGGGAGTTTGCAGTGACAGACCTGGCAAAATCCATTTG 1320
 Db |||||
 Qy 1321 GGATAAGCTCAATTTTCTAGGATTTGTTCTGATTGGAAGAGTGTCTTCTGTTCCCGC 1380
 Db |||||
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 Db |||||
 Qy 1381 TGTCTGTTCTTGTCAACCTTAACAAAGAGGACCGAATGAAAAATACCTGGAGACAGC 1440
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 Qy 1381 TGTCTGTTCTTGTCAACCTTAACAAAGAGGACCGAATGAAAAATACCTGGAGACAGC 1440
 Db |||||
 Qy 1441 AAGTGTAAATGTTGGGCTGGGCTGATGAGAGAGCTGTGTCGATTGCTCTTGTCTTACA 1500
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 Qy 1441 AAGTGTAAATGTTGGGCTGGGCTGATGAGAGAGCTGTGTCGATTGCTCTTGTCTTACA 1500
 Db |||||
 Qy 1501 ATAAATTTACAAATCTGGCCATCTCAGCTGCAACGGCAATGCAATATGATCACCAGCA 1560
 Db |||||
 Qy 1501 ATAAATTTACAAATCTGGCCATCTCAGCTGCAACGGCAATGCAATATGATCACCAGCA 1560
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 Qy 1561 CCATCAGTCTGTTCTTTTGTAGCACTATGTTTGGATGATGACAAAGCAATGATCA 1620
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 Qy 1561 CCATCAGTCTGTTCTTTTGTAGCACTATGTTTGGATGATGACAAAGCAATGATCA 1620
 Db |||||
 Qy 1621 GGCTGCTGCTACCGGCTCAGGCGCATCTGTCACCTCTGAGCCCTTCATCAACAAAGTCCC 1680
 Db |||||
 Qy 1621 GGCTGCTGCTACCGGCTCAGGCGCATCTGTCACCTCTGAGCCCTTCATCAACAAAGTCCC 1680
 Db |||||
 Qy 1681 TGCATTCTCTCTCTGACAAAGCATGCAAGGTTCTGACCTCGAGAGTACAAACCAATTTG 1740
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 Qy 1681 TGCATTCTCTCTCTGACAAAGCATGCAAGGTTCTGACCTCGAGAGTACAAACCAATTTG 1740
 Db |||||
 Qy 1741 TGAGGCTCTCCAGCTCGGATGCTCTCCCAAGCGACCCACACTGTCCACTACTACT 1800
 Db |||||
 Qy 1741 TGAGGCTCTCCAGCTCGGATGCTCTCCCAAGCGACCCACACTGTCCACTACTACT 1800
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 Qy 1801 GGCCCAAGTTCGACGAGCGCTGATGCGACCGATGTTTGGCGGCGGGTTCGTGCGCT 1860
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 Qy 1801 GGCCCAAGTTCGACGAGCGCTGATGCGACCGATGTTTGGCGGCGGGTTCGTGCGCT 1860
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 Qy 1861 TCTCCCTGGATCACCAACCGAGAGCCATGGAGGAAGATGAAACAGTGCAAAAGAAATG 1920

Db 1861 TCTCCCTCGGATCCCAACCGAGAGCCATGGAGGAATGAACAGTGCAGAAATG 1920
Qy 1921 AGAATGGAATGTTGATGAGAGAAATACATGTAATAATGTGACAGCAAAAGAGAGGCA 1980
Db 1921 AGAATGGAATGTTGATGAGAGAAATACATGTAATAATGTGACAGCAAAAGAGAGGCA 1980
Qy 1981 AGTTTGGGTTTGTAGAGTTGGCTGCTGCTAAATGAGTTGTTGATGCTGCTATATCTT 2040
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Qy 2101 TCGGATGATTGGTTGTTCTGTGAGGATGAACCTAGTGAAGTGAACAGAGGTTGATGTC 2160
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Qy 2161 TCCGACAACTGTAAATTTGTAGATTAAACAGCCCAATTTGTACTGTCTACCAATCTTTA 2220
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Qy 2281 TAGATTGTTGTATAATAATTTGCTTGTGTAATAAATAAATAAATAAATAAATAAATAA 2330
Db 2281 TAGATTGTTGTATAATAATTTGCTTGTGTAATAAATAAATAAATAAATAAATAAATAA 2330

RESULT 2

AAF75764

ID AAF75764 standard; DNA; 2423 BP.

AC AAF75764;

XX 14-MAY-2001 (first entry)

XX Gene regulating the pH of vacuoles.

XX Vacuole pH regulation; flower colour; ds.

XX Petunia hybrida.

XX WO200114560-A1.

XX 01-MAR-2001.

XX 24-AUG-2000; 2000WO-JP05722.

XX 24-AUG-1999; 99JP-0236800.

XX (SUNR) SUNTORY LTD.

XX Iida S, Tanaka S, Inagaki Y;

XX WPI; 2001-191648/19.

XX P-FSDB; AAB73252.

Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture -

XX Example 7; Page 37-42; 68pp; Japanese.

XX The present sequence is a gene, which encodes a protein with vacuolar pH regulatory activities. The gene enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The gene is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable

CC in horticulture.

XX Sequence 2423 BP; 621 A; 428 C; 518 G; 856 T; 0 other;
SQ

Query Match 34.1%; Score 793.4; DB 22; Length 2423;
Best Local Similarity 69.9%; Pred. No. 1e-208;
Matches 1089; Conservative 0; Mismatches 461; Indels 9; Gaps 1;

Qy 335 GTACAGACCTCCGACTACGCGTCGGTGGTGCATCAACCTGTTGTCGCGCTGCTCTG 394
Db 393 GTTATCGACATCTGATCATCAATCAGTTGTGTGCGATAAACTTATTCGTTGCTCTTATTG 452
Qy 395 CGCTCGCATCGTCTCGGCCACTCTCGAGGAGATCGCTGGGTCAATGAGTCCATCAC 454
Db 453 CGCGTGATTTGTGATCGGTCAATTTGTGAAGAAAACAGATGAGTGAATGATCCATAC 512
Qy 455 CGCGCTCATCATCGGCTCTGCACCGGCTGGTGTATCTTGTGTGATGACCAAGGGAAGAG 514
Db 513 TGCTTAGTGATGGTTCTTGTACTGGAATCGTTATCTACTGATAAGTGGAGGAAGAA 572
Qy 515 CTGCACTTATTCGTTTCAGTGAGGATCTCTTCTTCACTACCTCTCCCTCCGATCAT 574
Db 573 CTCTCATATTTTAGTGTTCAGTGAAGATCTTTTCTTCAATTTACCTTCTCCGCCAATCAT 632
Qy 575 CTTCAATGACGTTTTCAGTAAAGAAAAGCAATTTCTCCGGAATTTTCATGACGATCAC 634
Db 633 TTTTATGTCGGTTCAGGTGAAAAGAAATCGTTTCTTCCGCAATTTTCAGCACTATCAT 692
Qy 635 ATTATTTGAGCGCTCGGACAAATGATATCTTTTTTCAAAATCTATTGTCGCAATGCG 694
Db 693 GCTCTTTGGGCACTTGGCACCTTGATATCATTTATATATCATTAGGTGCCATTGG 752
Qy 695 AATATTCAGCAGAAATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTCAATTTGGAGC 754
Db 753 CATTTTCAAGAAAATGAATATTTGGAAGCCTTGAAATTTGAGATTTACCTTTGCAATTTGGGC 812
Qy 755 CATCTTTCTGCGACAGATTTCTGTCGCATTTGAGGTCCTCAATCAGGATGAGACACC 814
Db 813 AATCTTCTCTGTACAGATTTCTGTATGCACTTACAGTGTAAATCAGGATGAACACC 872
Qy 815 CTTTTGTACAGTCTGGTATTCGGTGAAGGTGTGTGAACGATGTCTACATCAATTTGTCT 874
Db 873 CTTATTTGACAGTCTAGTTTTTGGGGAAGGTGTTGTGATGATGCCACATCTGTAGTTCT 932
Qy 875 TTTCAAACGCACTACAGAACTTTTGAATCTTGTCCACATAGATGCGGTGTCGTTCTGAAAT 934
Db 933 GTTCAATGCTATCCAGAACTTTTGACTTATCTCACATCGACACGGGCAAGCTATGGAAT 992
Qy 935 CTTGGGGAACCTCTTTTATTTATTTTGTGAGCACCTTCTTGGAGTATTTGCTGGATT 994
Db 993 AGTTGGAACCTTTCTATACTTGTTTGCCCTCAAGCACTGCCCTAGGAGTTGCTGCGCCT 1052
Qy 995 GCTCAGTGCATACATAATCAAGAGCTATACATTTGAAGCATTCTTACTGACCGTGAGGT 1054
Db 1053 ACTGAGCGCTATATTTATTTAAATACTTACTTTGGAAGGCACTCACTGACCGTGAGGT 1112
Qy 1055 TGCCCTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCTGAGTTGCTAGATTTGAG 1114
Db 1113 TGCTAATGATACTCATGGCTTACCTATCTTACATGCTTGTGTAATTTCTTATTTAAG 1172
Qy 1115 CGGCATTTCCAGGTATTTCTTGTGGTATTTGTAATGTACATACACTTGGCATACAGT 1174
Db 1173 TGAATCTCCTGCTGTTTTTCTCTGGGATCGTGATGTCTCACTACACCTGGCATATGT 1232
Qy 1175 CACAGAGGTTCAAGAGTTTACAAAGCAGCATTTGCAACTCTGCTCTTCAATTCCTGA 1234
Db 1233 GACTGAGGCTCGAGAGTCACTACCAAGCACATTTTGTGTACATATATTTATTGCTGA 1292
Qy 1235 GACTTTTCTTCTCTGATTTGGGATGGATGGATTTGGAATTTGAAAAATGGAGTTTGC 1294
Db 1293 AATATTCATATTTCTTTATTTGTTGTTGATGATGCTTTGGGATTTGGAAGTGAAGTTTGT 1352
Qy 1295 CAGTGACAGACCTGGCAAAATCCATTTGGGTAAGCTCAATTTTGTAGGATTTGGTCTGAT 1354

Db	1353	AAGCAGAGCCCTGGAAATATCAGTTCAGGTTAGCTCAATATTGCTGGGCTGTGTTGGT	1412
Qy	1355	TGGAAGAGCTGCTTTTGTATTCCCGCTGCTGTTTGTGCGAACCTAAACAAAGAAAGGCACC	1414
Db	1413	TGGAAGAGCAGCATTTGTTTTCCTATGTCATTCCTGCCAATCTGACCAAGAAACTCC	1472
Qy	1415	GAATGAAAAAATAACCTGGAGACAGCAAGTTGTAATATGTTGGGTGGGGCTGATGAGAGG	1474
Db	1473	AGAGGCGAAAAATTAGTTTTAACACAGCAGGTTTCAATATGTTGGGTGGGACTTATGAGAGG	1532
Qy	1475	AGCTGTGCAATTCGCTTCCTGTCTACAAATAAGTTTACAAGATCTGGCCATATCTCAGCTGCA	1534
Db	1533	TGCGTTTCTATGCGCCTTGCTTTATTAATCAGTTTACAGGGAGGTCACTATCTAGTTACG	1592
Qy	1535	CGCAATGCAATAATGATCACACAGCACCATCTGCTGTTCTTTTAGCACTATGCGTATT	1594
Db	1593	CGCAAAATGCAATAATGATCACAAGTACTATCACTGTTGTCTCTTTTTCAGCACACGTCGT	1652
Qy	1595	TGGATGATCACAAAGCCATTGATCAGGCTGCTGCTACGGC-----CTCAGGCCA	1645
Db	1653	TGGTTGATGACAAAACCTTTGATTGAATAATTGCTACCTCACAAACACTTTGAGGAG	1712
Qy	1646	TCCTGTCACTCTGAGCCTTCATCACAAAGTCCCTGCAATTCCTCTCTCCAGCAAGCAT	1705
Db	1713	AATGATCTCTTCTGAAACCAAGACGCCAAAATCCCTTCATTGFGCCACTTCTTGACAGCAC	1772
Qy	1706	GCAAGGTTCTGACCTCGAGAGTACAACCAACATTGTGAGGCCCTCCAGCCTCCGGATGCT	1765
Db	1773	ACAAGACTCAGAAGCTGATCTGGAACGCCATGTACCCCGTCCCAACAGTTTGGCGGATGCT	1832
Qy	1766	CCTCACCAAGCCGACCCACACTGTCCACTACTACTGGGCGCAAGTTCGACGACGGCTGAT	1825
Db	1833	CCTTTCAACCCCATCTCATACAGTGCAATTATTACTTGGAGAAAGTTTGACATGCAATTCAT	1892
Qy	1826	GCACACGATGTTTGGCGGGCGGGGTTTCGTGCCCTTCTCCCTTGGATCAACAAACCGAGC	1884
Db	1893	GCCTCAGTTTTCGGTGGACGAGGTTTGTACTCTTTGCTCCAGATCACCGACAGACC	1951

RESULT 3
AAA72926
ID AAA72926 standard; DNA: 1668 BP.

AA
AC AAA72926:

XX

DT 23-NOV-2000 (first entry)

DE Atlixplex gmelini Na⁺ and H⁺ antiporter protein encoding DNA.

[illegible]

KW Atlixplex gmelini; Na plus and H plus antiporter protein;

KW Na⁺ and H⁺ antiporter prKW high salt tolerant
VV

Atliplex amelin

XX
03
УСТРХ УМЕТН

PN JP2000157287-A.

XX	5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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ED XX
13-JUN-2000.

PF 16-SEP-1999; 99JP-

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FR 24-SEP-1998; 98JUP-0269504.
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PA (SHOK-) SHOKUBUTSU KOGAKU KK.

XX 29

CC The present sequence encodes an Na⁺ and H⁺ antiporter protein isolated
CC from *AtHliplex gmelini*. The Na⁺ and H⁺ antiporter protein and gene
CC encoding it are useful for the preparation of transformed plants with
CC high salt tolerance, e.g. for growth in arid land.

Sequence 1668 BP; 397 A; 342 C; 376 G; 553 T; 0 other;

Query Match	34.0%;	Score 791.4;	DB 21;	Length 1668;
Best Local Similarity	70.0%;	Pred. No. 2.9e-208;		
Matches 1115; Conservative	0;	Mismatches 436;	Indels 42;	

339	QY	ACGACCTCGCACTACGCGTCGGTGTGTCATCAACCTGTTTCGTGCGCGTCTCTGCGCC	338
49	Db	ACCACCTTCGATCAGCGCTTCTGTGCTCTCGATGAACCTGTTGTGTGGCACTGTTATGTGGT	108
399	QY	TGCATCGTCTCTCGGCCACCTCTCGAGGAGAAATCGCTGGGTCAATGAGTCCATCACCGCG	458
109	Db	TGTATCGTAATTTGGTCACTCTTAGAGAGAAATGGTGGATGAATGAGTCAATCACTGCC	168
459	QY	CTCATCATCGGCTCTGCACGGCGTGTGTCTTGTGTATGACCAAGGGAAGAGCTCG	518
169	Db	CTTCTTATAGGTTTGGCTACTGGGCTTGTGATCTGCTGATTAGTGAGGAAAAAGTTCA	228
519	QY	CACCTATTGCTCTTCAGTGAGGATCTCTCTTCATCTACCTCCCTCCGATCACTTC	578
229	Db	CATCTTTTGGTCTTCAGTGAAGATCTTTTCTTCATATACCTTCTCCACGATATATTC	288
579	QY	AATGCAGGTTTTCAGTAAAGAAAAAGCAATCTTCCGGAAATTCATGACGATCACATTA	638
289	Db	AATGCAGGCTTTCAGGTGAAGNAGAGCAGTCTTTCGCACTTCATTAATTTGATTG	348
639	QY	TTTGGAGCGCTCGGACAAATGATATCTTTTTTCAAAATATCTATGCTGCCATTCGAATA	698
349	Db	TTTGGAGCTGTGTGTACATTTGGTATCATTCACCATCATATCTCTGGGAGCGTGTCAATT	408
699	QY	TTTCAGAGAAATGAACTTTGGBAACCTGGATGTAGAGATTTCTTTCGAAATGGAGCCATC	758
409	Db	TTTAAAGAAATTTGGATTTGGTACTCTGGAGTTGGCACTATCTTGCAATTTGGTGAATA	468
759	QY	TTTTCTGCGACAGATTTCTGTCTGCACATTCGAGGTCCTCAATCAGGATGAGACACCCCTTT	818
469	Db	TTTCGCTGCCACAGATTTCTGTTTGGCACACTGCAGGTTCCTTAATCAGGATGAGACCCCTCTG	528
819	QY	TTGTACAGTCTGGTATTCGGTGAAGGTGTGTGAAAGATGCTACATCAATTTGCTTTTC	878
529	Db	CTCTCAGTCTGGTCTTTTGGCGAGGTTGTGTAATGATCCACATCAGTGGTCTCTTTTC	588
879	QY	AACGCACTACAGAACTTTTGATCTTGCCACATAGATCGGCTGCTTCTGAAATCTCTG	938
589	Db	AATGCAATTCAGAGCTTTGACCTCACAGAATTCATCACAGATAGCTTTACAAATTAAG	648
939	QY	GGGAATCTCTTTTATTTATTTTGTGAGCACTTCTCTGGAGTATTTGCTGAGTGCCTC	998
649	Db	GGCAACTCTATATTTTATTTTATCGAAGCACGATACTTGGAGCATTTACTGGCTTCTC	708
999	QY	AGTGCAATCAATAATCAAGAGCTATACATTTGGAAGCAATTCCTACTGACCGTGAAGTTGCC	1058
709	Db	AGTGCTTCAATTTATCAAAAAGCTGTACTTTGGAAGGCATTTCCACTGATCGTGAAGTTGCT	768
1059	QY	CTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCTGAGTTGCTAGATTTTGAGCGGC	1118
769	Db	TTAAATGATGCTTATGGCTTATCTATCTTACATGCTTGTCTGNACTTTTCTATTTGAGTGA	828
1119	QY	ATTCTCACGGTATTTCTCTGTGGTATTTGTAATGTCAATTTACCTTTGGCATTAACGTCACA	1178
829	Db	ATTCTTACTGTATTTCTCTGTGGGATTTGTCATGTGCCATTTATACCTGGCAAAATGTGACA	888
1179	QY	GAGAGTTCAAGAGTTTACAACAAAGCAGCATTTTGCACACTCTGTCTCTTCAATTCGTGAGACT	1238
889	Db	GAGAGCTCAAGAGTAAACCAACAGCATGCTTTTTCACAACTATCTTTTGTGCTGAGTT	948
1239	QY	TTTCTCTTCTGTATTTTGGGATGGATGCAATTTGGATATTGAAAAATGGGAGTTTGGCAGT	1298

Db 1296 ATAATGATACTCATGGGTACCTATCATACATGCTGTGTAATTAATCTATTAAAGTGA 1355
Qy 1119 ATTCTCACGTAATCTCTGTGGTATTGTAATGTCACATTAACATTTGGCATAACGTCACA 1178
Db 1356 ATCCTCACTGTGTTTCTGTGGGATCGTATGCTCTCACTATACCTGGCATAATGTGACT 1415
Qy 1179 GAGAGTCAAGAGTTTACAACAGCAGCATTTGCAACTCTGTCTCTTCAATGCTGAGACT 1238
Db 1416 GAGAGCTCAAGAGTCACTACCAAGCACACGTTTGCTACATTATCATTTATTGCTGAAATA 1475
Qy 1239 TTTCTCTCTCTGTATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
Db 1476 TCTATTATCTCTTATGTTGGTATGATGCTTTGGACATTTGGAAGTGAAGTTTGAAGC 1535
Qy 1299 GACAGACCTGGCAATCCATTGGGATAAGCTCAATTTTGTAGGATGCTTCTGATGGA 1358
Db 1536 GACAGCCCGGAAACATCAATTAAGTCACTCAATTTCTGCTAGGCTTGTGTTGGTGA 1595
Qy 1359 AGAGTGTCTTTGTAATCCCGCTGTCTGTTGTCGAACTTAACAAAGAGCACCGAAT 1418
Db 1596 AGGGAGGCTTTGTTTCCCTTGTCAATCTGTCCAACTTGACCAAGAAAAATCCTGAG 1655
Qy 1419 GAAAAATAAAGCTGAGACAGCAAGTCTTAATATGCTGGCTGGCTGATGAGAGGCT 1478
Db 1656 GACAAGATTAGCTTTAACAGAGGTTTACAATATGTTGGGCTTATGCGAGGTGCT 1715
Qy 1479 GTGTGATGCTTGTCTTACAATAAGTTTACAAGATCTGGCCATPACTCAGCTGCACGCG 1538
Db 1716 GTTCTATGGCCCTTGTCTTATAATCAGTTTACCAGGGAGGTCACTACTCAGTTAGTGCC 1775
Qy 1539 AATGCAATAATGATCACAGCACCATCATCTGTCTGTTCTTTTAGCACTATGTTAGTGG 1598
Db 1776 AATGCAATAATGATCACAGTACTATCACTGTGTCTCTTTTTCAGCACAGTGTGTTGGG 1835
Qy 1599 ATGATGACAAAGCCTTATGATGAGGCTGTCTACCGGCTCAGGCTCCTCTCTCA ---- 1653
Db 1836 TTGATGACAAACCTTTAATCTATTATGCTTACCTCACAACAACTTGTATCAGAAATG 1895
Qy 1654 ----CCTCTGAGCCTTATCAACAAAGTCCCTGCAATCTCTCTCTGACAAAGCATGCAA 1709
Db 1896 ATCTCTCTGAACGATGACTCCAAATCTCTTCTTGTGTGCTTCTTGTGACGACACAA 1955
Qy 1710 GGTCTGACCTGAGAGTACACCAACATTTGTAGGCTTCCAGCTCCGATGCTCTCTC 1769
Db 1956 GACTCAGAAGCTGATCTGGGCGGACATGATCCCGTCCCGCAGTTTCCGATGCTCTCTG 2015
Qy 1770 ACCAAGCGACCCACACTGTCTCACTACTGCGGCAAGTTTCGACGCGCTGATGGA 1829
Db 2016 TCAACCCCATCTCACACGATCATTAATCTGAGAAATTTGACATGCAATTCATGCT 2075
Qy 1830 CCGATGTTTGGGCGCGGTTCTGTCCTTCTCTCCCTGGATCAACCAACGAGCAGAGC 1889
Db 2076 CTGTTTTCGTTGGAGAGGTTTGTACCTTTTGTTCAGGATCACCTACTGAACCGTCT 2135
Qy 1890 CA 1891
Db 2136 CA 2137

RESULT 5

AAZ22591

ID AAZ22591 standard; cDNA; 2178 BP.

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AC AAZ22591;

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DT 18-JAN-2000 (first entry)

XX

DE Arabidopsis thaliana Na/H transporter gene AtNHX1.

XX

KW Sodium; proton; antiport; transporter; salt tolerance; salt management;

KW transgenic plant; survival; soil; farming; accumulation; irrigation;

KW crop; ss.

XX

OS Arabidopsis thaliana.

XX PN WO9947679-A2.

XX PD 23-SEP-1999.

XX PF 18-MAR-1999; 99WO-CA00219.

XX PR 18-MAR-1998; 98US-0078474.

XX PR 15-JAN-1999; 99US-0116111.

XX XX (BLUM/) BLUMWALD E.

XX PA (APSE/) APSE M.

XX PA (SNED/) SNEDDEN W.

XX PA (AHAR/) AHARON G.

XX PI Blumwald E, Apse M, Snedden W, Aharon G;

XX XX WPI; 1999-571840/48.

XX DR P-PSDB; AAY40901.

XX XX

XX PT Nucleic acid molecules encoding sodium/proton transport polypeptides,

XX PS useful in genetic engineering salt tolerance in crop plants -

XX XX Claim 4; Fig 1A; 93pp; English.

XX CC

XX CC The invention relates to an isolated nucleic acid molecule encoding a

XX CC plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and

XX CC capable of increasing salt tolerance in a cell. This sequence corresponds

XX CC to the gene encoding the AtNHX1 transporter from Arabidopsis thaliana.

XX CC The Na/H transporter polypeptides provide a means of intracellular salt

XX CC management, particularly in plants. The sequences are useful for

XX CC producing transgenic plants that are capable of surviving in soil with

XX CC high salt levels that would normally inhibit growth of the crop species.

XX CC This would be useful in farming land in areas that are generally

XX CC considered unproductive through salt accumulation and poor irrigation,

XX CC e.g. in India, Australia, and prairies in USA or Canada. Commercial

XX CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,

XX CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, barley,

XX CC atriplex, sorghum, alfalfa, salicornia and others would benefit from

XX CC increased salt tolerance.

XX XX

XX SQ Sequence 2178 BP; 576 A; 413 C; 472 G; 717 T; 0 other;

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Db 452 CATTACTGCGCTTATAATTTGGTTTGTGACCGGAGTTGTAATTTTGGCTCCTTAGCGGAGG 511
Qy 509 GAAGAGCTCGCATTTATTCGCTTTCAGTGAGGATCTCTCTTCATCTACCTCCTCCCTCC 568
Db 512 AAAGAGTTCAACATCTTCTCGCTTTTAGGGAAGATCTTTTCTTTATATATCTCTGCCACC 571
Qy 569 GATCATCTTCAATGACAGGTTTTTCAGTAAAGAAAAGCAATTTCTTCCGGAATTTTCATGAC 628
Db 572 TATATATTCATGCGGGTTTCAAGTGAAAAGAGCAGTTTTTTCGTGAATTCATGAC 631
Qy 629 GATCATATTTTGGAGCGCTCGGACAAATGATATCTTTTTTCAAAATATCTATTGCTGC 688
Db 632 AATTATGCTGTTTGGAGCTATTGGACACATTTATTAGCTGTTCTATTATATCATTTTGGTGC 691
Qy 689 CATTGCAATATTCACGAGAAATGGAACATTTGGAACGCTGGATGAGAGATTTTCTTGCAAT 748
Db 692 GGTCAAAATTTTCAAGCACTTAGACATTTGCTTGTGATTTTGGAGATTTATTAGCAAT 751
Qy 749 TGGAGCCATCTTTTCTGGACAGATTTCTGCTGCACATTTGCAAGTCTCTCAATCAGGATGA 808
Db 752 TGGTGGATATTTGCTGAACCGATCTGTTTGGACATTTGCAAGTCTCTCAATCAGGATGA 811
Qy 809 GACACCTTTTGTACAGTCTGGTATTCGTTGAAGGTTGTTGGAAGATGCTACATCAAT 868
Db 812 GACGCCCTACTTTTACAGTCTGCTGTTTGGAGAGGGTCTGTCATGATGCTACATCTGT 871
Qy 869 TGTGTTTTTCAACGCACTACAGAACTTTGATCTTGTCTCCACATAGATCGGCTGCTGTTCT 928
Db 872 GGTCTTTTAAATGCTATTCAAAGTTTGAAGTCTAGTTTGTGATCAAAATTTGGGCT 931
Qy 929 GAAATCTTGGGAACTTCTTTTATTTATTTTGTGAGCACCTTCTTGGAGTATTTGC 988
Db 932 TCATTTCAATGGAACCTTCTGTTATTTATTTCTCTCGAGCACTTTTGGGCGTGGAAAT 991
Qy 989 TGGATGCTCAGTGCATACATAACGAAGCTATACATTTGAAGGCAATTTCTACTGACCG 1048
Db 992 TGGAGTCTTGTGCTTATATCAAAAGCTATACCTTTGGCAGGCACTCAACCGATCG 1051
Qy 1049 TGAGTTCGCCCTTATGATGCTCATGCTTACCTTTTATATATGCTGCTGAGTGTCTAGA 1108
Db 1052 TGAGTTCGCCCTTATGATGCTCATGCTTATGCTTATATATGCGGAGTATTTCTA 1111
Qy 1109 TTTGAGCGGCAATTTCTACCGTATTTCTTGTGTTATTTGATGTCACATTAACACTTGGCA 1168
Db 1112 TCTAAGCGGCATCTACTGTTATTTCTGTTGGAATTTGTCATGCTCTATTATACCTGCA 1171
Qy 1169 TAACTGCACAGAGTTCAAGAGTTACAACAAGCAGCATTTGCAACTCTGCTCTCAT 1228
Db 1172 CAATGTTTACCGAGAGCTCAAGGGTCACTACTAGGCAATTCCTTTGCAACTCTGCTATTGT 1231
Qy 1229 TGCTGAGACTTTTCTCTTCTGTTATGTTGGATGATGATTTGGAATTTGAAAATGGGA 1288
Db 1232 CGCAGAGACATTTATCTTCTATGTTGTTGATGATGCTTGGATTCGAGAAATGGA 1291
Qy 1289 GTTTGCCAGTGACAGACTGGGCAATCCATTTGGGTAAGCTCAATTTTGTAGGATGGT 1348
Db 1292 ATTTGTGAAAATAAGTACAGGCACTATCAGTTGCACTGAGCTCAATTTGGTAGGCCTAAT 1351
Qy 1349 TCTGATTTGGAAGAGCTGCTTTGTTATTTCCCGCTGCTGCTTCTTGTGCACTTAAACAAGAA 1408
Db 1352 CTTAGTAGGACAGAGCTGCGTTCGTTATTCCTTCTGCTTCTTATCCAACTTAGCAAGAA 1411
Qy 1409 GGCACCGAATGAAAATAAATCTGGAGACAGCAAGTTGCTATATGTTGGTGGCTGGCTGAT 1468
Db 1412 AAACCTTCGCAAGATATCTTTAGGCAACAAATAATATTTGGTGGCTGGCTTAAT 1471
Qy 1469 GAGAGAGCTGTGAGTGTCTTTGCTTACAATAAGTTTACAAGATCTGCCCATCTCA 1528
Db 1472 GAGAGGCGCGCTCTCAATAGACACTTGCATATAAATAAGTTTACAACCTCGGGGCATACGTC 1531
Qy 1529 GCTCAGCGCAATGCAATAATGATCACCAGCACCATCACTCTGTTCTTTTAGCACTAT 1588

Db 1532 ATTGCACGAGAACCAATAATGATTACAAGTACTGTTTACGGTGTGTTCTGTTTACGACAGT 1591
Qy 1589 GGTATTTGGGATGATGACAAAGCCATTGATCAGGCTGCTGTACCGG- - - - -CTCAG 1641
Db 1592 TGTATTCGGGTTGATGAGAAAGCTCTGATAAACCTTCTGCTACCCCGCAAGCAGAT 1651
Qy 1642 GCCATCTCTGTC- - - - -ACCTCTGAGCCTTTCATCAGCAAGTCCCTGCAATC 1687
Db 1652 GCCAAGCGGTCATTCGTCATGACAAATCGAACCCAGTAGTCCGAAGCACTTCACCGT 1711
Qy 1688 TCCTCTCTCTCAGAGCATGCAAGGTTCTGACCTCGAGAGTACAACCA- - - - -ACATGT 1741
Db 1712 GCCACTCTCTGACAAACCAACCTGACTCAGAAAGCATATGATAACCGGACCTGAGGTTGC 1771
Qy 1742 GAGCGCTTCCAGCCTCCGGATGCTCTCCACCAAGCCGACCCACACTGTCCTACTACTG 1801
Db 1772 TCGAACCACTGCCCTTGGCATGCTGTAAGACGCCAACCCACACCGTGCACCGTACTG 1831
Qy 1802 CGCAAGTTTCGACGACGCGCTGATCGCACCGATGTTTGGCGGGCGGCTTTCGTCGCCCTT 1861
Db 1832 CGGTAAGTTTGTATGCTTATGCGTCCGCTGTTTGGCGGGCGGGAATTCGTTCCGTT 1891
Qy 1862 CTCCCTCTGGATCAACAACGAGAGAGCCATGGAGGAGATGAA 1905
Db 1892 TGTCCGGGCTCACCAGTTGAGCAGAGCCCTAGATGAGGTACAA 1935

RESULT 7
AAZ22595
ID AAZ22595 standard; cDNA; 2284 BP.
XX AC AAZ22595;
XX AC
XX 18-JAN-2000 (first entry)
XX Arabidopsis thaliana Na/H transporter gene.
DE Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop; ss.
XX Arabidopsis thaliana.
XX
XX WO9947679-A2.
XX 23-SEP-1999.
XX 18-MAR-1999; 99WO-CA00219.
XX 18-MAR-1999; 98US-0078474.
XX 15-JAN-1999; 99US-0116111.
XX (BLUM/) BLUMWALD E.
XX (APSE/) APSE M.
XX (SNED/) SNEDDEN W.
XX (AHAR/) AHARON G.
XX Blumwald E, Apse M, Snedden W, Aharon G;
XX WPI; 1999-571840/48.
XX P-PSDB; AAY40905.
XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT useful in genetic engineering salt tolerance in crop plants -
XX Claim 48; Fig 5A-B; 93pp; English.
XX The invention relates to an isolated nucleic acid molecule encoding
CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
CC and capable of increasing salt tolerance in a cell. This sequence
CC corresponds to the gene encoding a transporter from Arabidopsis thaliana.
CC The Na/H transporter polypeptides provide a means of intracellular salt
CC management, particularly in plants. The sequences are useful for

XX

(SUNR) SUNTORY LTD.

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Iida S, Tanaka S, Inagaki Y;

XX

WPI, 2001-191648/19.

XX

P-PSDB; AAB73254.

XX

Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture

XX

Example 7; Page 53-57; 68pp; Japanese.

XX

The present sequence is a gene, which encodes a protein with vacuolar pH regulatory activities. The gene enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The gene is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.

XX

Sequence 2361 BP; 614 A; 468 C; 516 G; 763 T; 0 other;

SQ

Query Match

Best Local Similarity 30.5%; Score 711.8; DB 22; Length 2361;

Matches 1085; Conservative 0; Mismatches 507; Indels 39; Gaps 3;

QY

341 GACCTCCGACTACGGTCGGTGGTCTCCATCAACCTGTTCTGCGGCTGCTGCGCCTG 400

DB

449 GAGCTCTGGTCACGGTTTCAAGTGGTCCGTATACCTTATTTGTCACCTTCTCTGCACATG 508

QY

401 CATGCTCTCCGACACCTCTCGAGGAGAAATCGCTGGGTCAATGAGTCCATCACCGCGCT 460

DB

509 TATAGTGAATGGTCATCTTCTGGAGGAAAACGTTGGATGAATGAATCTATCATTTGCCCT 568

QY

461 CATCATCGGCTCTCACCGGCTGGTGAATCTTGTGATGACCAAGGAGAGAGCTCGCA 520

DB

569 CATAAATGGTTTACGACCGGGAGTTAATCTGTGTAATAGTGTGGAAGAGCTCCCA 628

QY

521 CTATTCTGCTTCACTGAGGATCTCTTCTCATCTACCTCTCCCTCCGATCATCTCAA 580

DB

629 TCTCTGGTTCAGTGAGATCTTTCTTCACTATGCGCTGCCACCAATCATTTTAA 688

QY

581 TGCAGTTTTCAGGTAAGAAAAGAAATCTTCCGGAATTTCAATGACGATCAATATT 640

DB

689 TCGGGGTTCCAAGTAAAGAAATCATTTCTTCCGAATTTGCAACTATAATGATGTT 748

QY

641 TGGAGCGCTCGGACAAATGATATCTTTTTCACAAATCTATTGCTGCCATTCGAATTT 700

DB

749 TGGAGCAGTTGGTATCTTGTATATCTTCAATCATCTTTTCACTCGGTACAAATGCAATCTT 808

QY

701 CAGCAGAAATGAACATTGGAACGCTGGATGATGAGAGATTTCTTCAATTTGGAGCCTCTT 760

DB

809 CCCAAATGAACATGAGA---CTTGGAGTTGGAGATTAATCTTGTATTTGGAGCTATTTT 865

QY

761 TCTGCGACAGATTTCTGTGCAATTCGAGTCTCTCAATCAGGATGAGACACCCCTTTT 820

DB

866 TGCTGCAACAGACTCAGTTTGCAATTAACAGTGTCTAAGCCAGGACGAAACACCACTGTT 925

QY

821 GTACAGTCTGATTTTCGTTGAAGTGTGTGAACGATGCTCATCAATTTGCTTTTCAA 880

DB

926 GTACAGTCTAGTTTGGCGAGGGTGTGTAATGACGCGACTTCAGTGGTCTTATTTAA 985

QY

881 CGCACTACAGAACTTTGATCTTGTCCATAGATGCGGCTGCTGCTTCTGAAATTTCTGGG 940

DB

986 TGCAGTACAGAACTTCGACCTGCCTCATATGTCTACTGCTAAAGCTTCGAGCTTGTGG 1045

QY

941 GAACTTCTTTTATTTATTTTGTGAGACCTTCTTCTGGAGTATTTGCTGGAATTTGCTCAG 1000

DB

1046 AAACCTCTTTTATTTATTTTGTCAAGCACTGTGCTGGGTGCTCTGACTGGAATGCTTAG 1105

QY

1001 TGCATACATATCAAGAAGCTATACATTTGGAAGCAATTTCTACTGACCGTGGAGTTGCCT 1060

Db 1106 TGCATACATCAAAAAAGCTCTATTTTGGAAAGGCACCTCCACTGATCGAGGTTGCCAT 1165

QY 1061 TATGATGCTCATGCTTACCTTTTATATATGCTGGCTGAGTTGCTAGATTTGAGCGGAT 1120

Db 1166 AATGATACTCATGGCTTATCTGTGTATATGTTAGCTGAATTTTCGATTTGAGCGGTAT 1225

QY 1121 TCTCACCTATTTCTGTGTATTTGTAATGTCACATTACACTTGGCATAAGCTCACAGA 1180

Db 1226 CCTCACCGTGTCTTCTGTGGAATTTGATGTCGCACCTATACATGGCACAATGTCACCTGA 1285

QY 1181 GAGTTCAAGATTACAAAGACGCAATTTGCAACTCTGCTCTTCTTCTGCTGAGACTTTT 1240

Db 1286 AAATCAAGAGTTTACCAAGCATACATTTGCGACATTTGCTTGTGCTGAAATATT 1345

QY 1241 TCTCTTCTGTATGTTGGGATGGATTCGATATGGAATATGAAAATGGGAGTTTGCAGTGA 1300

Db 1346 TATATTTCTGTATGTTGGCATGGATGCTTTAGACATTTGAGAAATGGAGATTTGCTAAGCGG 1405

QY 1301 CAGACCTGGCAAAATCCATTTGGGATAAGCTCAATTTTGTAGGATTTGTTCTGATTTGGAAG 1360

Db 1406 CAGCATGACAACATCTGCAGCTGTCAGTGCAACTCTGCTGGGATTTGTTTGTCTCAAG 1465

QY 1361 AGCTGCTTTTGTATTTCCGCTGCTGTTCTTGTGAACTTAACAAAGAGGCAACCGAATGA 1420

Db 1466 AGCAGCCTTTGTATTTCCCTTTTATCATTTCTCTCAATCTGGCCAAAAGTCCCACTCGA 1525

QY 1421 AAAAATAACCTGGAGACAGCAAGTTGTAATATGTTGGCTGGCTGATGAGAGGAGCTGT 1480

Db 1526 AAAAATCAGTCTCAGGAGCAAAATTAATAATGTTGGGCTGGTCTTATGCGGAGCGCT 1585

QY 1481 GTCAATGCTCTTCTTACAAATAGTTTAAAGATCTGGCCATCTCAGCTGCAAGCGCAA 1540

Db 1586 TTCCATGGCTCTTCTTACAGCAGTTTACTAGAGAGGCTCTCAGTGGAACGTTGAAA 1645

QY 1541 TGAATTAATGATACAGACCATCATCTGCTGTTCTTTTAAAGCTATGTTGATTTTGGAT 1600

Db 1646 TGCCATATTATCACCAGTACATCACCATTGCTCTTTCAGCACCTGTGTGTTTGTGTTT 1705

QY 1601 GATCACAAGGCATTGATCAGGCTGCTGTACCGGCTCTCAGGCCATCTCAGCTGCAAGCGCAA 1654

Db 1706 GATGACGAAGCCCTCATCAATTTACTGATACCTCACCAGCTTAAACAGATCGTCTC 1765

QY 1655 CTCTGAGCCTTTCATCACAAGTCCCTGCAATTCCTCTCTCTGACAAAGCATGCAAGGTTT 1714

Db 1766 TTCAGAACGCTGACTCCAACTCCATCAATCCCACTTCTCGGGGAAAGTCAAGGACTC 1825

QY 1715 TGACCTCGAGATACAAACCAACA-----TTGTGAG 1744

Db 1826 TGTGGCCGAACCTATTACGATCAGAGGTCAAACTTCAAGGTGGCGAACCCGTTGCTCG 1885

QY 1745 GCCTTTCAGCCTCGGATGCTCTCACAAGCGGACCCACACTGTCACACTACTACTGCGG 1804

Db 1886 ACCGAGCAGCTACGCAATGTTACTCACAAGCCCACTCATACGTTGCACTATTATTGGAG 1945

QY 1805 CAAGTTTCGACGACGCTGATGCGACCGGATGTTTGGGGGGCGGGTTTCGTCCTTCTC 1864

Db 1946 AAAATTCGACAAATGCTTTTATGCTCCGGTCTTTGTTGGGCTGCTGCTTTGACCATATGT 2005

QY 1865 CCTTGGATTCACCAACCGCAGCAGCCATGGAGGAAGATGAACAGTGCMAAGAAATGAGAA 1924

Db 2006 TCCCGGTTCCCGACTGAACGAAGCGTTTCGCACTGGGAAGAAGAGACCAACAGTAAAA 2065

QY 1925 TGAATGTTTG 1935

Db 2066 AGATTTCTTG 2076

RESULT 9

AAZ22592

ID AAZ22592 standard; cDNA; 1788 BP.

XX

AC AAZ22592;

XX 18-JAN-2000 (first entry)
 DT Arabidopsis thaliana Na/H transporter gene AtNHX2.
 DE
 XX Sodium; proton; antiport; transporter; salt tolerance; salt management;
 KW transgenic plant; survival; soil; farming; accumulation; irrigation;
 KW crop; ss.
 XX Arabidopsis thaliana.
 OS
 XX WO9947679-A2.
 PN
 XX 23-SEP-1999.
 PD
 XX 18-MAR-1999; 99WO-CA00219.
 PF
 XX 18-MAR-1998; 98US-0078474.
 PR 15-JAN-1999; 99US-0116111.
 PR
 XX (BLUM/) BLUMWALD E.
 PA (APSE/) APSE M.
 PA (SNED/) SNEDDEN W.
 PA (AHAR/) AHARON G.
 XX
 XX Blumwald E, Apse M, Snedden W, Aharon G;
 PI WPI; 1999-571840/48.
 XX P-PSDB; AAY40902.
 DR
 XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
 PT useful in genetic engineering salt tolerance in crop plants
 XX Claim 4; Fig 1B; 93pp; English.
 PS
 XX The invention relates to an isolated nucleic acid molecule encoding a
 CC plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and
 CC capable of increasing salt tolerance in a cell. This sequence corresponds
 CC to the gene encoding the AtNHX2 transporter from Arabidopsis thaliana.
 CC The Na/H transporter polypeptides provide a means of intracellular salt
 CC management, particularly in plants. The sequences are useful for
 CC producing transgenic plants that are capable of surviving in soil with
 CC high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 CC considered unproductive through salt accumulation and poor irrigation,
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,
 CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance.
 XX
 SQ Sequence 1788 BP; 475 A; 367 C; 370 G; 576 T; 0 other;

Query Match 21.8%; Score 508.8; DB 20; Length 1788;
 Best Local Similarity 62.7%; Pred. No. 5.2e-130;
 Matches 811; Conservative 0; Mismatches 477; Indels 6; Gaps 1;

Qy 346 CCGACTACGCTGGTGTGTCATCAACCTGTTCTGTCGGCTGCTCTGGCGCTGATCG 405
 Db 104 CTGAGCATCTTCAGTGNATCAATCTCAGTGTTCATCGCCATCTCTGTATGTTAG 163
 Qy 406 TCCTCGGCCACCTCCTCGAGGAGATCGTGGGTCAATGAGTCATCACCGCGCTCATCA 465
 Db 164 TTATCGGCCACTTGTCTTGAAGAGAATCGATGGGTTAATGAATCTATTACCGCCATTTAG 223
 Qy 466 TCGGCTCTGCACCGCGGTGTGATCTTGTGATGACCAAGGAGGAGCTCGCACTTAT 525
 Db 224 TAGGAGCAGCATCAGGACAGTGTATCTTACTTATAGTAAAGGAAAAGTTACATATTT 283
 Qy 526 TCGTCTTCAGTGAGGATCTCTTCTTCATCTACCTCCCTCCGATCATCTTCAATCGAG 585
 Db 284 TGGTGTGATGAGAACTCTCTTCATTTACCTTCTTCTCCCAATATCTTCAATGCTG 343

Qy 586 GTTTTCAGGTAAGAAAAGCAATTTCTTCGGAAATTTTCATGACGATCACATATTTCGAG 645
 Db 344 GGTTCCAAGTTAAGAAAAGAAAGTTTTTTCACAACTTTTAAACCATCATGTTCCTTGGTG 403
 Qy 646 CCGTCGGGACAAATGATATCTCTTTTTCACATATCTATTGTCGCCAATTCGAATATTCAGCA 705
 Db 404 TGATTGGAGTTTTTCATCTCCACTGTCTATCTCTGTTGGGACTTGGTGGCTGTTCCCA 463
 Qy 706 GAATGAACATTTGGAAACGCTGGATGTAGGAGATTTCTTGTGCAATTTGGAGCCATCTTTCTG 765
 Db 464 AGTTGGGATTTAAGGGGTTGAGTGTAGAGACTATCTTGCCATAGGAACGATTTTCTCAT 523
 Qy 766 CGACAGATTCGTCTGCACATTTGCAGGTCTCAATCAGGATGACAGACACCCCTTTTGTACA 825
 Db 524 CAACGTGATACCTGTTGCACTCTACAGATTTCCATCAAGATGAACACCACTGTCTATACA 583
 Qy 826 GTCTGGTATTCGGTGAAGGTGTGTGAACGATGCTACATCAATTTGTCTTTTCAACGCAC 885
 Db 584 GCTTAGTCTTTGGAGAGGAGTGTGTGATGATGCAACTCAGTTGTACTGTTCACGCCG 643
 Qy 886 TACAGAACTTTGATCTCTGTCACATAGATGCGGTGTCTGTTCTGAAATTTCTGGGGAAT 945
 Db 644 TGCAAAAGATTTCAATTTGAAAAGCCTAACCGGTTCGACGGCGCTGCAAGTATTTGGGAAT 703
 Qy 946 TCTTTTATTTATTTTGTGAGACACCTTCCTTGGAGTATTTGCTGGATGCTCAGTGCAT 1005
 Db 704 TTTTGTACCTCTCTCTCAACAAGCACACTTCTCGGAATTTGGTGGGGCTAATAACATCTT 763
 Qy 1006 ACATAATCAAGAAGCTATACATTTGGAAGGCATTTCTACTGACCGTGAGGTTCCTCTATGA 1065
 Db 764 TTGTTCTTTAAACCTTGTATTTTGGAGACATTTCTACTACAGCGAATCTGCCATCAGG 823
 Qy 1066 TGCTCATGCTTACCTTTTCATATATGCTGCTGAGTGTCTAGATTTGAGCGGCAATTTCTCA 1125
 Db 824 TTCTAATGGCTTACCTTTTCATATATGTTGGCTGAGCTCTTCTCATTAAGTGAATTTCTTA 883
 Qy 1126 CGGTATTTCTTGTGGTATTTGTAATGTCACATTAACATTTGCGCCTAATTCACAGAGTT 1185
 Db 884 CTGTTTTCTTCTGTGGTGTGTTTAAATGTGCGATTTATGCAATATTAACGTGACAGAGCT 943
 Qy 1186 CAAGAGTTTACAAACAGCAGCATTTGCAACTCTGCTCTCTCATTTCTGCTGAGACTTTTCTCT 1245
 Db 944 CAAGAATCACTTCCAGGATGTTATTTGCAATGTTGCTCTTTATTTGGGAGACATTCATAT 1003
 Qy 1246 TCCTGTATTTGGGATGGATTCGATTTGGAATTTGAAAAATGGGAGTTTCCAGTGACAGAC 1305
 Db 1004 TTCTGTATGTTGGAACAGATGCTCTTGATTTTACAAAGTGAAGACAAGCAGCTTAAGCT 1063
 Qy 1306 CTGGCAATCCATTTGGGATAGCTCAATTTGCTAGGATTTGTTCTGATTTGGAAGAGCTG 1365
 Db 1064 TTGGGGGTACTCTGGGTGTCTCCGGTGTCAACCGCATTTAGTATTTGCTTGGACGAGAG 1123
 Qy 1366 CTTTGTATTTCCGCTGTCTGTTCTTGTGGAACCTTAACAAAGAG-----GCACCGAATG 1419
 Db 1124 CATTTGTCTTTCATCTCTCGGCTTAAACAATTTTCATGACAGGCACACTGAAAGAACG 1183
 Qy 1420 AAAAAATAAACCCTGGAGACAGCAAGTTGTAATATGTTGGCTGGGCTGATGAGAGAGCTG 1479
 Db 1184 AGTCTATCACATTTAAGCATCAGGTGATCAATTTGGTGGGCGAGTCTAATTCGAGGTGCTG 1243
 Qy 1480 TGTGATTTGCTCTTCTTACATATAGTTTACAAAGATCTGGCCATCTCAGCTGCACGCCA 1539
 Db 1244 TCTCAATGCTCTGGCTTTCAAGCAGTTTCACATATCTCCGGTGTTCATATTGGATTCCTGTGA 1303
 Qy 1540 ATGCAATATGATCACAGCACCATCACTGTCTGTTCTTTTATAGCACTATGGTATTTGGGA 1599
 Db 1304 ATGTCGCAATGTCACCAACACCATATCTGTTGTTCTCTTTACTACACTGGTCTTTGGTT 1363
 Qy 1600 TGATGACAAAGCCATTTGATTCAGGCTGCTGCTACC 1633
 Db 1364 TCTCTCAAAACCACTTGTGAATTTATCTCTCTCC 1397

CC	polypeptides, in affinity purification of the polypeptides from	CC	recombinant cell culture or natural sources, and for inhibiting allergi
CC	reactions in animals. The present sequence encodes Physcomitrella patens	CC	Na+/H+ antiporter PpNHX1.
XX		XX	
XX	Sequence 1674 BP; 426 A; 350 C; 361 G; 537 T; 0 other;	XX	
DT		DT	
XX	Query Match	XX	20.7%; Score 482.8; DB 24; Length 1674;
XX	Best Local Similarity	XX	62.9%; Pred No. 7,8e-123;
XX	Matches 801; Conservative	XX	0; Mismatches 462; Indels 11; Gaps
XX		XX	
QY	360 GTGGTGTCATCAACCTGTTTCGTGCGTCTCTCGGCTGCATCTCTCGGCACCTTC	QY	360 GTGGTGTCATCAACCTGTTTCGTGCGTCTCTCGGCTGCATCTCTCGGCACCTTC
DB	79 GTAATTCAATCTGCTCTCTTTGTTTACTCTGTGCGTGCATTTGCTGGGACCTTT	DB	79 GTAATTCAATCTGCTCTCTTTGTTTACTCTGTGCGTGCATTTGCTGGGACCTTT
QY	420 CTCGAGGAATCGCTGGGTCAATGAGTCCATCAGCGGCTCATCATCGGGCTCTGCACC	QY	420 CTCGAGGAATCGCTGGGTCAATGAGTCCATCAGCGGCTCATCATCGGGCTCTGCACC
DB	139 CTGGAGGAAATCGGTGGATGAATGAGTCTATTACTGCTCTCTCTCTGAGACTTTT	DB	139 CTGGAGGAAATCGGTGGATGAATGAGTCTATTACTGCTCTCTCTCTGAGACTTTT
QY	480 GCGTGGTGATCTTCTGCTGATGACCAAGGGAAGAGCTGCACTTATTCTCTTCAGTGAG	QY	480 GCGTGGTGATCTTCTGCTGATGACCAAGGGAAGAGCTGCACTTATTCTCTTCAGTGAG
DB	199 GGATCTATAGTGTGATTTCAAGCAAGGTCAAGTTCATATTCTGGAGTTTCAAGAA	DB	199 GGATCTATAGTGTGATTTCAAGCAAGGTCAAGTTCATATTCTGGAGTTTCAAGAA
QY	540 GATCTCTTCTCATCTACCTCTCCCTCCGATCATCTTCAATSCAGGTTTTTCAGGTAAAG	QY	540 GATCTCTTCTCATCTACCTCTCCCTCCGATCATCTTCAATSCAGGTTTTTCAGGTAAAG
DB	259 GAGCTTTTCTCATATACCTCTCTCCACCTATAATCTCAATGCTGGTTCAGGTTAAG	DB	259 GAGCTTTTCTCATATACCTCTCTCCACCTATAATCTCAATGCTGGTTCAGGTTAAG
QY	600 AAAAGCAATCTCTCGGAAATTTCAAGAGTACATTTATTTGGAGCCGTCGGGACAATG	QY	600 AAAAGCAATCTCTCGGAAATTTCAAGAGTACATTTATTTGGAGCCGTCGGGACAATG
DB	319 AAGAAGGAATCTTTTCGGAAATTTCAACAATCATGTTTTTTGGAGTTTATAGGAGCTTT	DB	319 AAGAAGGAATCTTTTCGGAAATTTCAACAATCATGTTTTTTGGAGTTTATAGGAGCTTT
QY	660 ATATCTTTTTTCACAATATCTATTGCTGCCATTGCAATATTTCAGCAGAATGAACATTGGA	QY	660 ATATCTTTTTTCACAATATCTATTGCTGCCATTGCAATATTTCAGCAGAATGAACATTGGA
DB	379 ATTTCTTTTCGGAAATTTCTCAACAGAAAGTTGGTATTCTTCTCCAGTTCCGACTTAAG	DB	379 ATTTCTTTTCGGAAATTTCTCAACAGAAAGTTGGTATTCTTCTCCAGTTCCGACTTAAG
QY	720 AGCTGGATGTAGGAGATTTTCTGCCAATTTGGAGCCATCTTTTCTGCGACAGATTCTGTC	QY	720 AGCTGGATGTAGGAGATTTTCTGCCAATTTGGAGCCATCTTTTCTGCGACAGATTCTGTC
DB	439 AACCTGCCATTTCGAGATATCTAGCTATTGGAGTCACTTTTTCTGCTACCGATTCCGTC	DB	439 AACCTGCCATTTCGAGATATCTAGCTATTGGAGTCACTTTTTCTGCTACCGATTCCGTC
QY	780 TGCATTTGCAAGTCTCAATCAGGATGAGACACCCCTTTTGTACAGTCTGGTATTCGT	QY	780 TGCATTTGCAAGTCTCAATCAGGATGAGACACCCCTTTTGTACAGTCTGGTATTCGT
DB	499 TGCAGTTGCGAGGTGCTGAACCAAGATGAACCCCTCTACTTTACAGTTGGTCTTTGGG	DB	499 TGCAGTTGCGAGGTGCTGAACCAAGATGAACCCCTCTACTTTACAGTTGGTCTTTGGG
QY	840 GAAGTGTTGTGAACGATGCTACATCAATTTGCTTTTCAACGCACTACAGAACTTTGAT	QY	840 GAAGTGTTGTGAACGATGCTACATCAATTTGCTTTTCAACGCACTACAGAACTTTGAT
DB	559 GAAGGAGTCGTAATGATGCTACTTCTGTGTTCTGTCTCGAGCTGTTTCAACATACAC	DB	559 GAAGGAGTCGTAATGATGCTACTTCTGTGTTCTGTCTCGAGCTGTTTCAACATACAC
QY	900 CTTGTCCACATAGATGCGGCTGTCTGTTCTGAAATTTCTTTGGGAACTCTCTTTTATTTT	QY	900 CTTGTCCACATAGATGCGGCTGTCTGTTCTGAAATTTCTTTGGGAACTCTCTTTTATTTT
DB	619 TTTGCAAAATTTTACATCTTTAGAAGGCTTACAAATTTGAGGCGAGTTTCTGTACTTATTC	DB	619 TTTGCAAAATTTTACATCTTTAGAAGGCTTACAAATTTGAGGCGAGTTTCTGTACTTATTC
QY	960 TTGTTCGAGCACTTCTCTTTGGAGTATTTCGTGATTTGCTCAGTGATACATATCAAGAAG	QY	960 TTGTTCGAGCACTTCTCTTTGGAGTATTTCGTGATTTGCTCAGTGATACATATCAAGAAG
DB	679 TTCTCGAGTTGCATCTCTGGAAATCGCTCGGGCTTTAATGAAGCGCATATATCATCAAGAC	DB	679 TTCTCGAGTTGCATCTCTGGAAATCGCTCGGGCTTTAATGAAGCGCATATATCATCAAGAC
QY	1020 CTATACATTTGAAGGCATTTCTACTACCGTGAAGTTGCGCTTATGATGCTCATGCGCTTAC	QY	1020 CTATACATTTGAAGGCATTTCTACTACCGTGAAGTTGCGCTTATGATGCTCATGCGCTTAC
DB	739 ATGTACTTTGGCAGGCATTTCCAGGATCGTGAATAGCAATATGACATTTGATGCGGTAT	DB	739 ATGTACTTTGGCAGGCATTTCCAGGATCGTGAATAGCAATATGACATTTGATGCGGTAT
QY	1080 CTTTTCATATATGCTGGCTGAGTTGCTAGATTGTAGCGGCATTTCTCACCGTATTTCTTCTGT	QY	1080 CTTTTCATATATGCTGGCTGAGTTGCTAGATTGTAGCGGCATTTCTCACCGTATTTCTTCTGT
DB	799 TTATCTTACGCTTTTTCGAGAGCTTTTCTTACTTTGAGTGGAAATTTCTCAGTGTCTTTTTC	DB	799 TTATCTTACGCTTTTTCGAGAGCTTTTCTTACTTTGAGTGGAAATTTCTCAGTGTCTTTTTC
QY	1140 GGTATTGTAATGTACATTAACCTTGGCATACGTCACAGAGAGTTTCAAGAGTTTACAACA	QY	1140 GGTATTGTAATGTACATTAACCTTGGCATACGTCACAGAGAGTTTCAAGAGTTTACAACA
DB	859 GGCATTTGAATGTCTCTATTACATTTGGCATACCGTCACGAGAAATTTCTCGAATCAACAGC	DB	859 GGCATTTGAATGTCTCTATTACATTTGGCATACCGTCACGAGAAATTTCTCGAATCAACAGC
QY	1200 AAGCAGCATTTGCAACTCTGTCTTCTTCACTGAGAGCTTTTCTTCTCTCTCTCTCTCTCTCT	QY	1200 AAGCAGCATTTGCAACTCTGTCTTCTTCACTGAGAGCTTTTCTTCTCTCTCTCTCTCTCTCT
DB	919 AAGCATTCTTTGCAACGATGTCAATTCATTCGAGAGAGCTTCAATTTCTATATGTTGGA	DB	919 AAGCATTCTTTGCAACGATGTCAATTCATTCGAGAGAGCTTCAATTTCTATATGTTGGA
QY	1260 ATGGATGCAATTTGGATTTTGAATAATTTGGAGTTTGCAGTTGACAGACCTTGGCAATTTCCATT	QY	1260 ATGGATGCAATTTGGATTTTGAATAATTTGGAGTTTGCAGTTGACAGACCTTGGCAATTTCCATT

Db 979 ATGATGCTCTGGATTTCGAAAAATGAAGATGATGCAATCCAG-TTTCACGGAATCTGC 1037
Qy 1320 GGGATAAGCTCAATTTTGTAGGATTGGTCTCTGATTGGAAGAGCTGTTTGTATTTCCCG 1379
Db 1038 GGGCTATTGGTAGCTGTTGTTCTCTGCTCTGTAGGAGGGCGCAATTTGTGTTCCCA 1097
Qy 1380 CTGTCGTTTGTGCGAACCTTAACAAAGAGCGCACCGAATGAAAAATAAATACCTGGAGACAG 1439
Db 1098 CTCTCTGTTTGTGCAACTACAGCACAAAGTCTCCAGACGCGAAGATTATTTACGCCAA 1157
Qy 1440 CAAGTCTGAATATGGGCTGGGCTGATGAGAGAGCTGCTGTCGATGCTCTTGTCTAC 1499
Db 1158 ATGTTTATATCTGGTGGGCTGGACTAATGCGAGTCTGTCTCAATAGCACTGGCGTTC 1217
Qy 1500 AATAAGTTTACAGATCTGGCCATCTACTGATGACGCGCAATGCAATAATGATCACCAGC 1559
Db 1218 AACCAAG-----GGTGGTGTATGCAAGGCTCAACCAA-GCCAGGCTAATGGTCAIT 1267
Qy 1560 ACCATCACTGTCGTTCTTTTAGCACTATGTTTGGATGATGACAAAGCCATTTGATC 1619
Db 1268 ACTATCACTATGTCCTCTTTCAGCACTATTTGTTTGGCACTGTCACCAAGCCCTCTTATT 1327
Qy 1620 AGGCTGCTGCTACC 1633
Db 1328 AGTGGCTACTTCC 1341

RESULT 11

AAZ22606
ID AAZ22606 standard; DNA; 378 BP.
XX AC AAZ22606;
XX XX
XX XX
XX 18-JAN-2000 (first entry)
XX DE Rice Na/H antiport transporter gene from EST clone C91832.
XX Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop; ds.
XX OS Oryza sativa.
XX XX
XX WO9947679-A2.
XX XX
XX 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-CA00219.
XX PR 18-MAR-1998; 98US-0078474.
XX PR 15-JAN-1999; 99US-0116111.
XX XX (BLUM/) BLUMWALD E.
XX PA (APSE/) APSE M.
XX PA (SNED/) SNEDDEN W.
XX PA (AHAR/) AHARON G.
XX XX
XX Blumwald E, Apse M, Snedden W, Aharon G;
XX WPI; 1999-571840/48.
XX XX
XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT useful in genetic engineering salt tolerance in crop plants -
XX XX
XX Disclosure; Fig 8C; 93pp; English.
XX XX
XX The invention relates to an isolated nucleic acid molecule encoding
CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
CC and capable of increasing salt tolerance in a cell. This sequence
CC corresponds to an Na/H antiport transporter gene fragment from the
CC rice expressed sequence tag (EST) library clone AAC91832. The Na/H
CC transporter polypeptides provide a means of intracellular salt
CC management, particularly in plants. The sequences are useful for

CC producing transgenic plants that are capable of surviving in soil
CC with high salt levels that would normally inhibit growth of the crop
CC species. This would be useful in farming land in areas that are
CC generally considered unproductive through salt accumulation and poor
CC irrigation, e.g. in India, Australia, and prairies in USA or Canada.
CC Commercial crops, such as potatoes, tomatoes, brassica, cotton, wheat,
CC sunflower, strawberries, spinach, lettuce, rice, soybean, corn, alfalfa,
CC rye, barley, atriplex, sorghum, alfalfa, salicornia and others would
CC benefit from increased salt tolerance.

XX Sequence 378 BP; 88 A; 74 C; 89 G; 121 T; 6 other;

Query Match 14.6%; Score 340.4; DB 20; Length 378;

Best Local Similarity 95.0%; Pred. No. 8.7e-84;

Matches 359; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

Qy 1013 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGGTGGCTTATGATGCTCAT 1072
Db 1 CAAGAAGCTATACATTGGAAGGCATTCTACTGACCGTGGTGGCTTATGATGCTCAT 60
Qy 1073 GGCCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCATTCTCACCGTATT 1132
Db 61 GGCCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCATTCTCACCGTATT 120
Qy 1133 CTTCTGTGTTTGAATGTCATATTACATTGCGCATTAACGTCACAGAGATTCAAGAGT 1192
Db 121 CTTCTGTGTTTGAATGTCATATTACATTGCGCATTAACGTCACAGAGATTCAAGAGT 180
Qy 1193 TACAAACAAGCAGCATTTGCAACTCTCTCTTCACTGAGACTTTCTCTCTCTCTCTCTA 1252
Db 181 TACAAACAAGCAGCATTTGCAACTCTCTCTTCACTGAGACTTTCTCTCTCTCTCTCTA 240
Qy 1253 TGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312
Db 241 TGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 1313 ATCCATTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1370
Db 301 ATCCATTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 1371 GTATTCCCGCTGCTGCTC 1388
Db 361 GNAATTCCTGCTGCTGCTC 378

RESULT 12

AAZ22611
ID AAZ22611 standard; DNA; 330 BP.

XX AC AAZ22611;

XX DT 18-JAN-2000 (first entry)

XX XX

XX DE Arabidopsis Na/H antiport transporter gene from EST clone T75860.

XX Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop; ss.

XX OS Arabidopsis thaliana.

XX PN WO9947679-A2.

XX XX

XX PD 23-SEP-1999.

XX PF 18-MAR-1999; 99WO-CA00219.

XX PR 18-MAR-1998; 98US-0078474.

XX PR 15-JAN-1999; 99US-0116111.

XX XX (BLUM/) BLUMWALD E.

XX PA (APSE/) APSE M.

XX PA (SNED/) SNEDDEN W.

PA (AHAR/) AHARON G.
XX Blumwald E, Apse M, Snedden W, Aharon G;
XX WPI; 1999-571840/48.
XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT useful in genetic engineering salt tolerance in crop plants -
XX Disclosure; Fig 8H; 93pp; English.
XX The invention relates to an isolated nucleic acid molecule encoding
CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
CC and capable of increasing salt tolerance in a cell. This sequence
CC corresponds to an Na/H antiport transporter gene fragment from the
CC Arabidopsis expressed sequence tag (EST) library clone AAT75860. The
CC Na/H transporter polypeptides provide a means of intracellular salt
CC management, particularly in plants. The sequences are useful for
CC producing transgenic plants that are capable of surviving in soil
CC with high salt levels that would normally inhibit growth of the crop
CC species. This would be useful in farming land in areas that are
CC generally considered unproductive through salt accumulation and poor
CC irrigation, e.g. in India, Australia, and prairies in USA or Canada.
CC Commercial crops, such as potatoes, tomatoes, brassica, cotton, wheat,
CC sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat,
CC rye, barley, atriplex, sorghum, alfalfa, salicornia and others would
CC benefit from increased salt tolerance.
XX Sequence 330 BP; 92 A; 68 C; 66 G; 91 T; 13 other;
SQ
Query Match 6.0%; Score 139.2; DB 20; Length 330;
Best Local Similarity 65.9%; Pred. No. 4e-28;
Matches 195; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 1374 TTCCGCTGCTCTTCTCGAAGCTTACAAAGAGGACCGCAATGAAAATACCTGG 1433
Db 1 TTTCGGTATCGTTCTTCTATCTAATCCAGAGAAATCAAGCGAAATCAACTTT 60
QY 1434 AGACAGCAAGTTGTAATATGGTGGCTGGCTGATGAGAGAGCTGTCTCGATGCTCTT 1493
Db 61 AACATGCAGGTTGTGATTTGGTGTCTGCTCATGAGAGGTGTCTATCTATGCTCTT 120
QY 1494 GCTTACATAGTTTACAGATCTGGCCATCTAGCTGACGGCAATGCAATATGATC 1553
Db 121 GCATACAAAGTTTACAAAGGCGCGGCACACAGATGTACGNGGGAATGCAATCATGATC 180
QY 1554 ACCAGCACCATCACTGTCTTCTTTTACCACTATGTTATTTGGATGATGACAAAGCCA 1613
Db 181 ACGNGTAGCTAATCTGCTGTTTTTTTACCAAGTGGTGTGTTGGTATGCTGACCAACCA 240
QY 1614 TTGATCAGGCTGCTGCTACCGGCTCAGGCCATCTGTGACCTCTGAGCCCTTCATC 1669
Db 241 NTCATAGCTACCTATTATACGNAACCAAGACCGTCATCAACGNGCATGTTATC 296
RESULT 13
ABL73323
ID ABL73323 standard; cDNA; 281 BP.
XX ABL73323;
XX ABL73323;
DT 14-MAY-2002 (first entry)
DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:2697.
XX
XX Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPS;
KW inheritance; characteristic; growth; development; disease resistance;
KW environmental adaptability; quality; yield; molecular marker;
KW multigene trait; plant breeding; corn tassel; gene; ss.
XX
XX Zea mays.
XX
XX US2001051335-A1.

XX 13-DEC-2001.
XX 16-APR-1999; 99US-0294093.
XX 21-APR-1998; 98US-082567P.
XX (LALG/) LALGUDI R V.
PA (ITOL/) ITO L Y.
PA (SHER/) SHERMAN B K.
XX Lalgudi RV, Ito LY, Sherman BK;
XX WPI; 2002-163647/21.
XX Novel purified corn tassel-derived polynucleotide useful for
PT determining altered gene expression, to recover regulatory elements and
PT to follow inheritance of desirable characteristics through hybrid
PT breeding programs -
XX Claim 1; SEQ ID 2697; 201pp; English.
XX The present sequence describes a purified corn tassel-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL70627 to ABL76833. The cdps sequences
CC encode corn tassel-derived polypeptides (CDPS). The cdps sequences (I)
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (I) are also useful
CC in the evaluation, and alteration of desired characteristics associated
CC with growth and development, disease resistance, environmental
CC adaptability, quality and yield, and as molecular markers for studying
CC inheritance of multigene traits in a plant breeding program. (I) can be
CC used to produce a tassel-specific profile of gene transcription, a
CC transcript image, to clone regulatory elements for use in transformation
CC vectors, to express a polypeptide, to identify, isolate or extend
CC identical or related corn tassel nucleic acid sequences from DNA
CC libraries, in nucleic acid hybridization or amplification technologies,
CC as query sequences to determine homology of known sequences, as probe
CC for use in Southern or Northern hybridisation, and to identify the
CC presence of and/or to determine the degree of similarity between two
CC (or more) nucleic acid sequences.
XX SQ Sequence 281 BP; 83 A; 54 C; 56 G; 87 T; 1 other;
Query Match 6.0%; Score 138.8; DB 24; Length 281;
Best Local Similarity 72.5%; Pred. No. 4.7e-28;
Matches 208; Conservative 0; Mismatches 73; Indels 6; Gaps 2;
QY 1029 GGAAGGCATTCTACTGACCGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTCATAT 1088
Db 1 GNCAGACATTCAACTGATAGAGAAGTTTCTATCATGATCATCTCATGGCATACCTTTCATAC 60
QY 1089 ATGCTGGCTGAGTTGCTAGATTGAGCGGCATTCTACCGTATTTCTTCTGTGGTATTGTA 1148
Db 61 ATGATATCAATGCTGTTGGACCTGAGTGGAAATCTTACTGCTTCTTCTGTGGAAATAGTA 120
QY 1149 ATGTCACATTACACTTGGCATAAGCTCACAGAGAGTTTCAAGAGTTTACAAAGACGCA 1208
Db 121 ATGTCACATTACACTTGGCATAATGTGACAGAAAGTTTCTAGGGTTTACCAACATACT 180
QY 1209 TTTTGCAACTCTGCTCTTTCATTGCTGAGACTTTTCTCTCTGTATGTTGGATGGATGCA 1268
Db 181 TTTTGCAACTTT---ATCATCATGACAGAAATTTCTCTCTCTATGTTGGATGGATGCA 236
QY 1269 TTGGATATTGAAAATGGGAGTTTGCACAGTACAGACCTGGCAATC 1315
Db 237 T--GGACATGAGAAGTGGAAATTAGCTAGTAGCAGTCTCTAAGAAACC 281
RESULT 14
AAC95372
ID AAC95372 standard; cDNA; 1824 BP.

AC AAC95372;
 DT 19-FEB-2001 (first entry)
 DE Cat flea HMT Na/H transporter cDNA ORF, SEQ ID NO:1870.
 XX
 XX Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
 XX flea infestation; vaccine; antiparasitic; therapeutic target;
 KW diagnosis; detection; ss.
 KW
 XX Ctenocephalides felis.
 XX WO200061621-A2.
 PN
 XX
 XX 19-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-US09437.
 XX
 XX 09-APR-1999; 99US-0128704.
 XX (HESK-) HESKA CORP.
 PA
 XX Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
 PI WPI; 2000-656323/63.
 DR P-PSDB; AAB29621.
 DR
 XX
 XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic
 PT acids useful for the prevention, diagnosis and treatment of flea
 PT infestations -
 XX
 PS Claim 1; Page 894-895; 964pp; English.
 XX
 CC The invention relates to novel cat flea (*Ctenocephalides felis*) nucleic
 CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
 CC or head and nerve cord (HNC) tissue. The invention also relates to the
 CC encoded proteins. The invention additionally encompasses expression
 CC constructs, recombinant viruses and recombinant cells comprising the
 CC nucleic acids of the invention, recombinant production of the proteins,
 CC antibodies against the proteins, a method of identifying inhibitors of
 CC the proteins, and compositions comprising the inhibitors for
 CC administration to an animal. The nucleic acids, and the proteins they
 CC encode may be used in the prevention, treatment and diagnosis of diseases
 CC associated with flea infestations. For example, the nucleic acids may be
 CC used to produce an HMT or HNC protein according to standard recombinant
 CC DNA methodology by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
 CC and quantitate the presence of cat flea or other homologous nucleic acid
 CC sequences in samples. They may also be used to study the expression and
 CC function of the proteins and their role in metabolism. The HMT and HNC
 CC proteins may be used as antigens in the production of specific
 CC antibodies, and in assays to identify modulators (agonists and
 CC antagonists) of HMT and/or HNC protein expression and activity. The
 CC anti-HMT/HNC protein antibodies and antagonists may also be used to
 CC downregulate protein expression and activity. The antibodies may also be
 CC used as diagnostic agents for detecting the presence of flea polypeptides
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
 CC present sequence represents a cat flea HMT cDNA of the invention.
 XX
 SQ Sequence 1824 BP; 529 A; 330 C; 355 G; 610 T; 0 other;
 Query Match 4.7%; Score 109.4; DB 21; Length 1824;
 Best Local Similarity 47.8%; Pred. No. 1.9e-19;
 Matches 351; Conservative 0; Mismatches 381; Indels 3; Gaps 1;
 KY 546 TTCTTTCATCTACCTCCCTCCGATCATCTTCAATGAGGTTTTCAGGTAAAGAAAAG 605
 Db 445 TTTTCTTAGTCTCTACCGCTATAATTTGAATCCGGGTATATTTTCATAAAGGT 504
 KY 606 CAAATCTTCGGAAATTTTATGACGATACATATTTTGGAGCGGTGCGGACATATATCC 665
 Db 505 AATTTTTCAAAATATGTTGTTCCATCTCTGGTGTGTTGCTATATTTTGGAAACAGCATATCA 564
 QY 666 TTTTTCACAAATATCTATTTGCTGCCAATTCGAATATTTCAGCAGAAATGAACATTTGGAAACGCTG 725
 Db 565 GCCTTTGTTGTCGGTGTGTTGTTTACTAGGAATGGCAGATGTTGCTTATAACTTA 624
 QY 726 GATGTAGAGAGATTTTCTTGAATTTGGAGCCCATCTTTCTTGGCAGACAGATTCGTCTGCACA 785
 Db 625 AGCTTTGTTGAATCCTTTGCTTTTCCGTTTCATTAATTTCTGCAGTAGACCCCTGTAGTACC 684
 QY 786 TTGAGGTCCTCAA--TCAGGATGAGACACCCCTTTTGTGTACAGTCTGGTATTCCGGTGAA 842
 Db 685 GTAGCTATTTTCCATGCTTTAGACGTGGACCCAGTTTAAACATGTTGGTTCGGAGAA 744
 QY 843 GGTGTTGTGAACGATGCTACATCAATTTGTCTTTTAAACGCACTACAGAACTTTGATCTT 902
 Db 745 AGTATTTTAAATGATGCTATTTTCAATTTGTTTAAACAACTGCAGTTTGGMAATCCAACAT 804
 QY 903 GTCCACATAGATGCGGCTGCTGTTCTGAAATTTCTTGGGGAACCTTTTATTTATTTTGG 962
 Db 805 CCTTTAATGACGACTGCTGTAAGCTGTAGTCTCCGTTTAAATAGGTTTGTGTTTAAATGTT 864
 QY 963 TCGAGCACCTTCTTGGAGTATTTGCTGGAATGCTCAGTGCATACATAATCAAGAAAGCTA 1022
 Db 865 TTTGCTTCGGCTGTATCGGTGTAGTCTTTGCTTAATTTAGTGTCTTTTGTGAACAT 924
 QY 1023 TACATTTGGAAGCAATTTACTACCGTGCAGGTGCGCTTATGATGCTCATGGCTTACCTT 1082
 Db 925 GTTGATCTTGAAGAATATCCGTTAGAGTTAGGTATGATGTTGGTGTGTTTACTTATGCA 984
 QY 1083 TCATATATGCTGGCTGAGTTGCTAGATTTGAGCGGCATTTCTACCGTATTTCTCTGTGGT 1142
 Db 985 CCTTATGTTTGGCAGAGAAATTCATTTATCAGGTATAATGGCGATATTTCTGTGGC 1044
 QY 1143 ATTGTAATGTCACTTACACTTTGGCATTAACGTCACAGAGAGTTCAAGAGTTTACACAAAG 1202
 Db 1045 ATTGTAATGTCCATACACATTTCAATTTATCAACGGTTACACAAATAACTATGCGAG 1104
 QY 1203 CACGCAATTTGCAACTCTGTCTTCAATCTGAGACTTTTCTCTCTGTATGTTGGGATG 1262
 Db 1105 CAGACGATGAGAACTTGGCTTTTATTCAGAAACTTGTGTGTTTGTCTTATTTAGGAATG 1164
 QY 1263 GATGCAATTTGATATT 1277
 Db 1165 GCTATATTTAGTTTT 1179
 RESULT 15
 AAC95373/c
 ID AAC95373 standard; cDNA; 1824 BP.
 XX
 AC AAC95373;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Cat flea HMT Na/H transporter cDNA ORF complement, SEQ ID NO:1871.
 XX
 KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
 KW flea infestation; vaccine; antiparasitic; therapeutic target;
 KW diagnosis; detection; ss.
 XX
 OS Ctenocephalides felis.
 XX
 PN WO200061621-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-US09437.
 XX
 XX 09-APR-1999; 99US-0128704.
 XX (HESK-) HESKA CORP.
 PA
 XX

PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

AA
DR
WPI; 2000-656323/63.

DR P-PSDB; AAB29621.

Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea infestations -

PS Claim 1; Page 895-896; 964pp; English.

The invention relates to novel cat flea (*Ctenocephalides felis*) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HNC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, antibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and function of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific antibodies, and in assays to identify modulators (agonists and antagonists) of HMT and/or HNC protein expression and activity. The anti-HMT/HNC protein antibodies and antagonists may also be used to downregulate protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT cDNA of the invention.

Sequence 1824 BP; 610 A; 355 C; 330 G; 529 T; 0 other;

Query Match 4.7%; Score 109.4; DB 21; Length 1824;

Best Local Similarity 47.8%; Pred. No. 1.9e-19;
Matches 351; Conservative 0; Mismatches 381; Indels 3; Gaps 1;

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      1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 84
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QY 546 TTCTTCATCTACCTCCTCCTCCGATCATCTTCAATGCAGTTTTCAGTAAAGAAAAG 605

Db 1380 TTTTCTTAGTGTTCTACCGCTATAATTTGAATCCGGGTAAATTTGGTAAAGGT 1321

QY 606 CAATTCTTCGGGAATTCATGACGATCACATTATTTGGAGCCGTCGGGACAATGATATCC 665

Db 1320 AATTTTTCAAAATATTGGTTCATCCTGGTGTTCCTATATTGGAAACAGCCATATCA 1261

QY 666 TTTTTCACAATATCTATTGCTGCCATTGCAATATTCAGCAGAAATGAACATTGGAAACGCTG 725

Db 1260 GCCTTGTGTCGGTGCTGGTGTGTATTTACTAGGAATGGCAGATGTTGCTTATAACCTTA 1201

726 GATGTAGGAGATTTTCTTGGCAATTGGAGGCAATCTTTTCTGGCAGAGATTCTGTCTCCACA 785

1200 AGCTTGTGAATCCTTTGGTTTCCGTTCTTAAATTTCTGCACCTACCCCTCTCCCTACC 1143

OV 786 TTGCAGGTCTCAA ---TCAGGCAATGCACACACCCCTTTTCTTCACACTCCTCATTTCCCCCA 843

b6
b7C
b7D

1140 GTAGCTATTTTCCATGCGGTACGACGGGACCAAGTTTTAAACAATTGTCCTGCGGCAG

[illegible][illegible][illegible][illegible][illegible]

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match 1.9%; Score 44.6; DB 2; Length 32207;
Best Local Similarity 50.7%; Pred. No. 0.065;
Matches 107; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 368 CATCAACCTGTTGTCGGCTGCTCTGGCGCTGATCGTCTCGGCCACCTCTCGAGGA 427
|||||
Db 20748 CATCTCTCTGCTCATTTGCTCTCATCATCGTCTCTGCTCTCTCTCTCTCTCTCT 20807
QY 428 GAATCGTGGGTCAATGATGATCATACCGGCTCATCGGGCTCTCGACGGGGTGT 487
|||||
Db 20808 CCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20867
QY 488 GATCTTGTGCTGATGACAAAGGAGAGTCGCACTTATTCGTTTCAGTGAGGATCTCTT 547
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Db 20868 CATCTCTCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20927
QY 548 CTTCATCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 578
|||||
Db 20928 CATCTCTCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20958

RESULT 6
US-08-757-669A-20
Sequence 20, Application US/0875769A
Patent No. 6183751
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20

Query Match 1.9%; Score 44.6; DB 4; Length 32207;
Best Local Similarity 50.7%; Pred. No. 0.065;
Matches 107; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 368 CATCAACCTGTTGTCGGCTGCTCTGGCGCTGATCGTCTCGGCCACCTCTCGAGGA 427
|||||
Db 20748 CATCTCTCTGCTCATTTGCTCTCATCATCGTCTCTGCTCTCTCTCTCTCTCTCT 20807
QY 428 GAATCGTGGGTCAATGATGATCATACCGGCTCATCGGGCTCTCGACGGGGTGT 487
|||||
Db 20808 CCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20867
QY 488 GATCTTGTGCTGATGACAAAGGAGAGTCGCACTTATTCGTTTCAGTGAGGATCTCTT 547
|||||
Db 20868 CATCTCTCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20927
QY 548 CTTCATCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 578
|||||
Db 20928 CATCTCTCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20958

RESULT 7
US-09-230-371A-20
Sequence 20, Application US/09230371A
Patent No. 6348586
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 32207
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20

Query Match 1.9%; Score 44.6; DB 4; Length 32207;
Best Local Similarity 50.7%; Pred. No. 0.065;
Matches 107; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 368 CATCAACCTGTTGTCGGCTGCTCTGGCGCTGATCGTCTCGGCCACCTCTCGAGGA 427
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Db 20748 CATCTCTCTGCTCATTTGCTCTCATCATCGTCTCTGCTCTCTCTCTCTCTCTCT 20807

Query Match 1.8%; Score 42.4; DB 4; Length 68750;
Best Local Similarity 49.5%; Pred. No. 0.44;
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 311 GCGCGCGCGCGCTGGGGCTCTGTACACGACCTCCGACTACGCGTGGTGTGTCAT 370
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QY 371 CAACCTGTTCTCGCGTCTCTCGCTGTATCGTCTCGGCACCTCTCGAGGAGAA 430
DB 4410 CGCGCGCTCGCGCGCGCTCTCGCGGCTCAGGGGACGAGCGCGCTCTGGCGGT 4469

QY 431 TCGCTGGTCAATGAGTCCATCACCGCGCTCATCGGCTCTGACCGCGCTGTGAT 490
DB 4470 GGGCTGAACATGAAGGCGCGACCTCATCGTCGATCTCGCGCTCGAGCTCGG 4529

QY 491 CTTCGTGATGACCAAGGAAGAGCTCGCACTTATTGTC 530
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RESULT 14
US-09-568-486-1
; Sequence 1, Application US/09568486
; Patent No. 635459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-486-1

Query Match 1.8%; Score 42.4; DB 4; Length 68750;
Best Local Similarity 49.5%; Pred. No. 0.44;
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 311 GCGCGCGCGCGCTGGGGCTCTGTACACGACCTCCGACTACGCGTGGTGTGTCAT 370
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QY 371 CAACCTGTTCTCGCGTCTCTCGCTGTATCGTCTCGGCACCTCTCGAGGAGAA 430
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QY 431 TCGCTGGTCAATGAGTCCATCACCGCGCTCATCGGCTCTGACCGCGCTGTGAT 490
DB 4470 GGGCTGAACATGAAGGCGCGACCTCATCGTCGATCTCGCGCTCGAGCTCGG 4529

QY 491 CTTCGTGATGACCAAGGAAGAGCTCGCACTTATTGTC 530
DB 4530 GCTCCTCTCCAACGAGGCTTATACGATGTACGCGCTCGTC 4569

RESULT 15
US-09-568-472-1
; Sequence 1, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:

; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-472-1

Query Match 1.8%; Score 42.4; DB 4; Length 68750;
Best Local Similarity 49.5%; Pred. No. 0.44;
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 311 GCGCGCGCGCGCTGGGGCTCTGTACACGACCTCCGACTACGCGTGGTGTGTCAT 370
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QY 371 CAACCTGTTCTCGCGTCTCTCGCTGTATCGTCTCGGCACCTCTCGAGGAGAA 430
DB 4410 CGCGCGCTCGCGCGCGCTCTCGCGGCTCAGGGGACGAGCGCGCTCTGGCGGT 4469

QY 431 TCGCTGGTCAATGAGTCCATCACCGCGCTCATCGGCTCTGACCGCGCTGTGAT 490
DB 4470 GGGCTGAACATGAAGGCGCGACCTCATCGTCGATCTCGCGCTCGAGCTCGG 4529

QY 491 CTTCGTGATGACCAAGGAAGAGCTCGCACTTATTGTC 530
DB 4530 GCTCCTCTCCAACGAGGCTTATACGATGTACGCGCTCGTC 4569

Search completed: April 5, 2003, 15:59:11
Job time : 288 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Title: US-09-888-035A-1

Perfect score: 2330

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Scoring table: IDENTITY NUC

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Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	711	30.5	2066	9	US-10-155-535-3
4	138.8	6.0	281	10	US-09-294-093B-2697
5	77	3.3	1800	9	US-10-155-535-5
6	66.8	2.9	1688	10	US-09-800-729-57
7	65	2.8	1581	10	US-09-800-729-22
8	58.4	2.5	4598	9	US-09-822-846-118
9	52.4	2.2	1354	10	US-09-800-729-58
10	51.4	2.2	1935	9	US-10-217-096-3
11	51.4	2.2	3537	9	US-10-217-096-1
12	44.4	1.9	1305	10	US-09-815-242-7730
13	43.4	1.9	1883	12	US-10-033-109-9
14	43	1.8	690	10	US-09-887-576-816
15	42.6	1.8	325	9	US-10-040-739-929
16	42.6	1.8	88421	9	US-09-976-059-1
17	42.4	1.8	68750	9	US-10-014-717-1
18	41.2	1.8	1827	10	US-09-887-576-817
19	41	1.8	520	9	US-10-184-644-332

20	40.4	1.7	984	10	US-09-815-242-7872	Sequence 7872, Ap
21	40	1.7	916	9	US-10-184-644-78	Sequence 78, Appl
22	40	1.7	22960	10	US-09-070-927A-345	Sequence 345, App
23	39.8	1.7	2248	9	US-10-125-237-11	Sequence 11, Appl
24	39.6	1.7	1413	10	US-09-805-467A-1	Sequence 1, Appli
25	39.6	1.7	1461	9	US-10-006-950-1	Sequence 1, Appli
26	39.6	1.7	2300	10	US-09-805-467A-3	Sequence 3, Appli
27	39.4	1.7	747	10	US-09-887-576-781	Sequence 781, App
28	39.4	1.7	774	10	US-09-770-445-902	Sequence 902, App
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31	39.4	1.7	2625	12	US-10-023-673-1	Sequence 1, Appli
32	39.2	1.7	1898	10	US-09-768-826-22	Sequence 22, Appl
33	38.8	1.7	431	10	US-09-864-761-23962	Sequence 23962, A
34	38.8	1.7	573	10	US-09-864-761-7231	Sequence 7231, Ap
35	38.8	1.7	1758	10	US-09-815-242-7825	Sequence 7825, Ap
36	38.8	1.7	1944	10	US-09-864-761-2825	Sequence 2825, Ap
37	38.8	1.7	3826	10	US-09-927-091-3	Sequence 3, Appli
38	38.8	1.7	23433	10	US-09-927-091-3	Sequence 7, Appli
39	38.6	1.7	795	9	US-10-051-643-46	Sequence 46, Appl
40	38.6	1.7	795	9	US-09-880-505-46	Sequence 1, Appli
41	38.6	1.7	2040	10	US-09-733-300-1	Sequence 12, Appl
42	38.6	1.7	2040	10	US-09-733-300-1	Sequence 1, Appli
43	38.6	1.7	2080	9	US-10-003-392-1	Sequence 949, App
44	38.4	1.6	5431	10	US-09-834-375-949	Sequence 28059, A
45	38.2	1.6	327	10	US-09-864-761-28059	

ALIGNMENTS

RESULT 1

US-09-938-842A-1239

; Sequence 1239, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE OF INVENTION: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1239

; LENGTH: 1617

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1239

Query Match 33.0%; Score 768.8; DB 9; Length 1617;

Best Local Similarity 68.6%; Pred. No. 4.7e-230;

Matches 1077; Conservative 0; Mismatches 487; Indels 6; Gaps 1;

QY 329 GGCTCTGTACACGACCTCCGACTACCGCTCGGTGGTGTCCATCAACCTGTCGCGCT 388

Db 27 GCCTTCGTTATCGACATCTGATCAGCTTCTGTGGTGGTGAATCTCTTTGTTGCACT 86

QY 389 GCTCTCGGCTGATCGTCTCGGCCACCTCTCTCGAGGAGATCGTGGGTCAATGATC 448

Db 87 TCTTTGCTGTGTTATGTTCTTGGTTCATCTTTTGAAGAGATAGATGATGAACGAATC 146

QY 449 CATCACCGGCTCATCATCGGCTCTGACCGCGGTGATCTTCTGATGATCAACCAAGG 508

Db 147 CATCACCGGCTTGTGATTTGGCTAGGCATGTTTACCAITTTTGTGATTAGTAAGG 206

Qy 509 GAAGAGCTGGCACTTATTCGTCTTCAGTCAGGATCTCTCTTCTATCTACCTCCTCCTCC 568
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Qy 207 AAAAGCTCGCATCTTCGTCTTTAGTGAAGATCTTTCTTCTATATATCTTTGGCCACC 266
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Qy 569 GATCATCTTCAATGACAGGTTTTCAGTAAAGAAAAGCAATCTTCCGGAATTTCAATGAC 628
Db |||||
Qy 267 CATTTATTTCAATGACAGGTTTCAAGTAAAGAAAAGCAGATTTTCCGCAATTTGGTGAC 326
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Qy 629 GATCACATTTATTTGAGCGCTCGGACCAATGATATCTCTTTTCACAATATCTATTGCTGC 688
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Qy 327 TATTATGCTTTTGGTCTTGGGACATATTTCTTGCACAATCATCTCTAGGGTGT 386
Db |||||
Qy 689 CATTTCAATATTTGACGAGAAATGAACATTTGGAACGCTGGATGTAGGAGATTTCTTTGCAAT 748
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Qy 749 TGGACCACTTTCTTTCGACAGATTTCTGTCTGACATTTGACGCTTCAATCAGGATGA 808
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Qy 447 TGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTGTCAGGTTCTGAATCAAGACGA 506
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Qy 809 GACACCTTTTGTACAGTCTCGTATTCGGTGAAGGTGTGTGAACGATGTACATCAAT 868
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Qy 507 GACACCTTTGCTTTAAGTCTTGTATTCGGAGAGGTTGTGTGAATGATGCAACGTCAGT 566
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Qy 869 TGTGCTTTTCAACGCACTACGAACTTTGATCTTGTCCACATAGATGGGCTGTCTGTTCT 928
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Qy 567 TGTGCTTCTCAACGCACTTTCAGAGCTTTGATCTCACTCACTCACTCACTCACTCACTCACT 526
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Qy 929 GAAATCTTTGGGAACTTCTTTATTTATTTTGTGTCGAGCCTTCTCTTGGAGTATTTGC 988
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Qy 989 TGGATTGCTCAGTACATCAATCAAGAGCTATACATTTGGAAGGCACTTCTACTGACCG 1048
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Qy 1049 TGAGTTGCCCTTATGATGCTCATGGCTTACCTTTTCAATATGCTGGGTGATGCTCTAGA 1108
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Qy 1409 GGCACCGAATGAAATAAATTAACCTGGAGACAGCAAGTTGTAATATGTTGGGCTGGGCTGAT 1468
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Qy 1107 GAATCAAGAGCAGAAATCAACTTTTAAATGCAAGTGTGATTTGGTGTCTGCTGCTCAT 1166
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Qy 1589 GGTATTTGGGATGATGACAAAGCCATTTGATCAGGCTGCTGCTACCGGCTCAGGCGCATCC 1648
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Qy 1649 TGTCACTCTCTGAGCCTTCAATCAACAAAGTCTCTGCAATCTCTCTCTCTGCAAG 1702
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Qy 1703 CATCAAGGTTCTGACCTCGAGAGTACAAACCAATGTTGAGGCTTCCAGCCTCCGGAT 1762
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Qy 1407 AGACTGCTTCAATGAGCCTTCAGGAAACCAATGTTGCTCGGCTGACAGTATACGTGG 1466
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Qy 1823 GATCGGACCGATGTTTGGCGGGCGGGGTTCTGTCCTTCTCTCTCTGATCACCACCGA 1882
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; Sequence 1, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apse, Maris
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPOETERS
; FILE REFERENCE: 529152000720
; CURRENT APPLICATION NUMBER: US/10/155,535
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-155-535-1
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Best Local Similarity 69.1%; Pred. No. 2.5e-229;
Matches 1088; Conservative 0; Mismatches 462; Indels 24; Gaps 2;
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Db 1724 CGAGTATGTTATTCGACGATAGCACTCCGAAATCAATTCACATTTCCGCTCTCTCGATGGT 1783

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Db 1844 TTTGAGGTTTCTCTCATGCGCCCCACACGAGCTGTCTACTTACTTGGAGACAGTTTGATG 1903
Qy 1816 ACGCGCTGATGCGACCGATGTTTGGCGGCGGGTTCGTGCCCTTCTCCCTGTGATCAC 1875
Db 1904 ATGCTTTCAAGGCTCTGTGTTGTGCGGATTCGTTCCCTTTGCTCTGCTTCTC 1963
Qy 1876 CAACGAGCAGAGC 1889
Db 1964 CGACTGAGAGAGC 1977

RESULT 3
US-10-155-535-3
; Sequence 3, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apse, Maris
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; FILE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS
; FILE REFERENCE: 52915200720
; CURRENT APPLICATION NUMBER: US/10/155,535
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-155-535-3

Query Match 30.5%; Score 711; DB 9; Length 2066;
Best Local Similarity 65.8%; Pred No. 7, 7e-212;
Matches 1054; Conservative 0; Mismatches 540; Indels 9; Gaps 1;

Qy 343 CCTCCGACTACCGTGGTGGTGTCCATCAACCTGTTGTCGCGTGTCTGCGCTGCA 402
Db 50 CTTCTGATCATGCTCGTGGTCTCCATGAAATTTGTTGTTAGCTTTGTTGCTTGA 109
Qy 403 TGTCTCTCGGCACCTCTCGAGGAGATCGTGGTCAATGAGTCCATCAGCGGCTCA 462
Db 110 TGTGCTTGGTCACTTGTCTTGAGGAGACTCGGTGATGAACGAGTCAATCTGCTCTTA 169
Qy 463 TCATCGGCTCTGCAACCGCGTGGTGTCTTCTGATGACCAAGGAGAGCTCGCACT 522
Db 170 TCATTTGTTCTGTTACTGAGATTTGATCTGTTTATAGTGGAGGCAAAAGCTCAAGA 229
Qy 523 TATTCGTTCTGAGTGGAGTCTCTTCTTCACTACCTCTCTCCCTCGATCATCTTCAATG 582
Db 230 TTTCTGTTGTTAGTGAAGATCTCTTCTTATTTATCTTCTTCCACCAATTTATTTCAAG 289
Qy 583 CAGGTTTTTCAGGTAAAGAAAAAGCAATTTCTCCGAAATTTTCATGAGCATCAATTATTG 642
Db 290 CAGGTTTTTCAGGTAAAGAAAAAGCAATTTTTCGAACTTTCATGACCAATTTATTTTGG 349
Qy 643 GAGCGTTTCGGAACAATGATATCTTTTTCACAAATCTATTTCTGCTTGCATTTGCAATTTCA 702
Db 350 GTGCTATTGGAACCTCTCAATTTCAATTTGTTATCTATCTATTTGTTGTTGCTAAACATCTTTG 409
Qy 703 GCAGATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTCAATTTGGAGCCATCTTTT 762

Db 410 AGAAATGAATATCGGTGATCTTACCATTCGGGAGCTATCTAGCCATTCGGAGCAATATTTCT 469
Qy 763 CTGGACAGATCTCTCTGCAATTCGAGGTCTCAATCAGGATGAGACACCCCTTTTGT 822
Db 470 CTGCTACAGACTCTGTTGCACTTTCAGAGTCTTAATCAAGACGAGACACCTCTTGT 529
Qy 823 ACAGTCTGGTATTCGGTGAAGGTGTGTGAACGATGCTACATCAATTTGTGCTTTTCAACG 882
Db 530 ACAGTCTTGTCTTTGGAGAAGGTGTAGTGAACGATGCCACATCGGTCTGTCTCTTCAATG 589
Qy 883 CACTACAGAACTTTGATCTTGTCCACATAGATGCGGCTGTCTGAAATTTCTTTGGGA 942
Db 590 CAATACAGAGATTCGACCTCAAAATATCAATTCAGCCATAGCTTTGAGTTTGTGGAA 649
Qy 943 ACTCTTTTATTTATTTTGTGACACCTCTCTTTGGAGTATTTCTGCTGATTTGCTCAGTG 1002
Db 650 ACTTTTTTACCTCTTATCTTAACACAGACACTTGTGTTGTCAGTGTGATTTGCTCAGTG 709
Qy 1003 CATACATATCAAGAAGCTATACATTTGAAGGCACTTCTACTGACCGTGAGGTTGCCCTTA 1062
Db 710 CTTTGTGTTATCAAGAAGCTCTATATAGGAAGCACTTACTGATCGTGAAGTTGCACCTA 769
Qy 1063 TGATGCTCATGCTTACCTTTTCATATATGCTGGCTGAGTGTGCTAGATTTGAGCGCATTC 1122
Db 770 TGATGCTATTTGCTTACTTATCATATATGTTGGCAGAGCTATTCACCTTGAGCTCTATCT 829
Qy 1123 TCACCGTATCTTCTGTGTTGATTTGATGTCACATTTGACATTAACGTCACAGAGA 1182
Db 830 TGACTGTGTTCTTCTGCGGATGTTATGTTCTACATATACATGGCACAATGTTACAGATA 889
Qy 1183 GTTCAAGAGTTACAAACAAAGCAGCATTTGCAACTCTGTCTTCAATTTGCTGAGACTTTTC 1242
Db 890 AATCAAGGTCACATACAAAACATCTTTTGTGTCATGTCATTTCTAGCTGAGATTTTA 949
Qy 1243 TCTTCTCTATGTTGGGATGATGCAITGGATATTTGAAATGGAGTTTGGCAGTGACA 1302
Db 950 TCTTCTCTTACGTTGGAATGAGCGCTCTCGATATCGAGAAATGGGACGTTGTACGCAACA 1009
Qy 1303 GACCTGGCAAAATCCATTTGGGATAAGCTCAATTTTCTAGGATTTGTTCTGATTTGGAAGAG 1362
Db 1010 GTCTGTGTCAGTCGATTTGAGTGTAGTTCAATCTTCTTTGGGCTTATCTTCTGGTCTCGC 1069
Qy 1363 CTGCTTTTGTATTCCTGCTGTGTTGTGCAACTTAACAAAGAACCCAGATGAAA 1422
Db 1070 CCGGCTTCTGTTTCCACTTTCCTTCTGTCCAATTTAAACAAAGTCTTCAACGGATGAGA 1129
Qy 1423 AAATAACCTGGAGACAGCAAGTTGTAATATGGTGGCTGGGCTGATGAGAGAGCTGTGT 1482
Db 1130 AAATAGACTTAAAGAAACAAGTAACCAATTTGGTGGGCTGGTCTGATGCTGTGTGCAAGTGT 1189
Qy 1483 CGATTGCTCTTGTCTTACAAATAGTTTACAAGATCTGGCCATCTCAGCTGCACGGCAATG 1542
Db 1190 CAATGGCTCTTGTCTTATTAACAGTTTCAACCTTCAAGGACACACCAAGGTTCTTGGGAACG 1249
Qy 1543 CAATAATGATCAACAGCACCACTGCTGTTCTTTTATAGCACTATGTTATTTGGGATGA 1602
Db 1250 CTATCATGATCACAGTACCACTCACTGTGTTCTTTTCACTACTGTGTGTTTGGATTGC 1309
Qy 1603 TGACAAAGCCATTTGATCAGGCTGCTGCTACCGGCTCAGGCCATCTCTCACTCTGAGC 1662
Db 1310 TAAACAAACCGTTAGTCAAAATTTGACGCTTCTATCAAAACAGTCTCCACGACCCGCGC 1369
Qy 1663 -----CTTCATCACAAAGTCCCTGCAATTTCTCTCTCTGACAGCATGCAAGGTT 1713
Db 1370 TGCAGATCACACTAAGATCTTCTTCCACGATCCGATCTCTCATGAGCGGTTGTCAGTA 1429
Qy 1714 CTGACCTCGAGAGTACAAACCAATTTGAGGCTTCCAGCTCCGAGTCTCTCAACCA 1773
Db 1430 CCCAAGGCCAGTCAGAAATACCAACCCCTGAACCAACATGTTAGCTTCAGAAATGTTCTGGAAT 1489
Qy 1774 AGCCGACCCACACTCTCCACTACTACTGCGCAAGTTTCGACGCGCTGATGCGACGA 1833

Db 1490 CTCGCTCAGGCGCCATTCATCATTTACTGGAGAAATTCGATAACGCACTTATGCTCGCA 1549
Qy 1834 TGTTTGGCGGCGCGGGTTCGTGCGCTTCTCCCTGGATCACCAACCGAGAGAGCCATG 1893
Db 1850 TATTTGGTGGCGGAGCGCTTTCACCACTAGTTTCAGGTTTCAACCATTTAGAAATAGTGTTC 1609
Qy 1894 GAGGAAGATGAACAGTGCAGAGTGCAGAAATGAGAAATGGAATGGAATGTTGA 1936
Db 1610 CGCAATGGAGTGAAGAGTAGAAAAACAAGGAACAAACGCGGA 1652

RESULT 4
US-09-294-093B-2697
; Sequence 2697, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Laludi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 2697
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700346512H1
; NAME/KEY: unsure
; LOCATION: 2
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-2697

Query Match 6.0%; Score 138.8; DB 10; Length 281;
Best Local Similarity 72.5%; Pred. No. 5.3e-33;
Matches 208; Conservative 0; Mismatches 73; Indels 6; Gaps 2;
Qy 1029 GGAAGGCACTTCTACTGACCGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTCAAT 1088
Db 1 GNCAGACATTCAACTGATAGAGAGTTTCTATCATGATACTCATGGCATACTTTCTATAC 60
Qy 1089 ATGCTGGCTGAGTTGCTAGATTGAGCGGCATTTCTACCGTATTTCTTCTGTGGTATTGTA 1148
Db 61 ATGATATCAATGCTGTGAGACCTGAGTGAATTTCTTACTGTCTTCTTCTGTGGAAATAGTA 120
Qy 1149 ATGTCACATTACACTTGGCATAACGTCACAGAGAGTTTCAAGAGTTTACAACAAACGCGCA 1208
Db 121 ATGTCACATTACACTTGGCATAATGTGACAGAAAGTTCTAGGGTTTACCAACAGCATACT 180
Qy 1209 TTTGCAACTCTGTCTTCTTCAATGCTGAGACTTTTCTTCTCTGTATGTTGGATGGATGCA 1268
Db 181 TTTGCAACTTT----ATCATCATGACAGAAATTTCTCTCTCTATGTTGGATGGATGCA 236
Qy 1269 TTGATATTGAAATATGGGAGTTTGGCAGTGACAGACTTGGCAATTC 1315
Db 237 T--GGACATGAGAGTGGAAATAGCTTAGTAGCAGTCTTAAGAAACC 281

RESULT 5
US-10-155-535-5
; Sequence 5, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apse, Maris
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; EXPRESSION OF VACUOLAR CATION-PROTON ANTI-PORTERS

Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22

LENGTH: 1581
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (112)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (959)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1565)
OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-22

Query Match 2.8%; Score 65; DB 10; Length 1581;
Best Local Similarity 46.6%; Pred. No. 2.7e-09;
Matches 357; Conservative 6; Mismatches 367; Indels 36; Gaps 4;

Qy 531 TTCAGTGGAGGATCTCTTCTCATCTACCTCCCTCCGATCATCTTCAATGCGAGTTT 590
Db |||||
Qy 425 TTCGATCAGAGTATTTTTCAGATTCTCTGCTCCAAATTTTTCATGCTGGATAC 484
Db |||||
Qy 591 CAGGTAAGAAAAGCAATCTTCCGGAATTTTCAGCATCACATTAATTTGGAGCCGTC 650
Db |||||
Qy 485 AGCTTAAAGAAAGAGACACTTTTTCAGAAATCTTGGATCTATCTGCTGCCTATGCTTCTG 544
Qy 651 GGGCAATGATATCTTTTTCACATATCTATTGCTGCCATGCAATTCAGCAGATG 710
Db |||||
Qy 545 GGGAGCTGCTKTTTCACTGCTTCAATTAATTTGGAATCTCATGTATGCTGGTGAAGCTCATG 604
Qy 711 AACATTGGAACGCTGGATGTAGG-----AGATTTTCTTGCATTTGGAGCC 755
Db |||||
Qy 605 AAGATTATGGACAGCTCTCAGATAAATTTTACTACAGATGKCTCTTTTGGAGCA 664
Qy 756 ATCTTTTTCGACAGATTTCTGCTGCAATTCAGAGTCCCTCAATCAGGATGAGACACC 815
Db |||||
Qy 665 ATCATCTCTGCCACTGACCCAGTCACTGTGCTGGCGATATTTAATGAATTCATGCAGAC 724
Qy 816 TT---TTTGTACAGTCTGGTATTCGTTGAAGTGTGTTGAACGATGCTACATCAATTTG 872
Db |||||
Qy 725 GTGATCTTTACGCACTCTCTTTTGGAGAGCGCTTAAATGATGCTGTGGCCATGKA 784
Qy 873 C-----TTTCAACGCACTACAGAACTTTGTATCTGTCCACATAGATGCG 917
Db |||||
Qy 785 CTGKCTCGTCTATTGTTGGCTACAGCCAGCGGACTGACACTCAGCGCTTTGATGCT 844
Qy 918 GCTGCTGTTTGAATTTCTGGGAACTTCTTTTATTTATTTTGTGAGCACCTTCTT 977
Db |||||
Qy 845 GCTGCTTTTATAGTCAATTTTGGCAATTTTCTAGGTATATTTAGTGGCTCTTTTACCATG 904
Qy 978 GGAGTATTTGCTGGATGCTCAGTGCATACATAATCAAGAGCTATACATTTGGAAGCAT 1037
Db |||||
Qy 905 GGAGCTGTACTGTTGTGACTGC-----TCYAGTACTAAGTTTACCAACKGCAACNGC 961
Qy 1038 TCTACTACCGGTGAGTTGCCCTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCT 1097
Db |||||
Qy 962 TTCCCTGCTGGAGACGGGCTGTTCTCTCATGCTCTGAGCAGCTTTCTCTTGCA 1021
Db |||||

Qy 1098 GAGTTGCTAGATTTTACGGCAATTTCCCGTATTTCTTCTGTGGTATTTGTAATGTACAT 1157
Db |||||
Qy 1022 GAAGCTCGGATTTTACAGGTTTGTAGCTGCTCTTCTGTGGAATCACACAAGCTCAT 1081
Db |||||
Qy 1158 TACACTTGGCATACGTCACAGAGTTTCAAGAGTTTACAAAGACGCGATTTTCAACT 1217
Db |||||
Qy 1082 TACACTTACAAATCTGTCGGTGAATCAAGAAGTCGAACCAAGCAGCTCTTTGAGGTG 1141
Qy 1218 CTGTCCTTCATTTGCTGAGACTTTTCTCTCTGTATGTTGGATGG 1263
Db |||||
Qy 1142 TTACATTTCTGGCAGAGAACTTTCATCTTCTCATATGGGCTGG 1187

RESULT 8

US-09-822-846-118/c
; Sequence 118, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 4598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-118

Query Match 2.5%; Score 58.4; DB 9; Length 4598;
Best Local Similarity 46.8%; Pred. No. 7.2e-07;
Matches 354; Conservative 0; Mismatches 366; Indels 36; Gaps 4;
Qy 540 GATCTCTTCTCATCTACCTCCCTCCGATCATCTTCAATGAGGTTTTCAGGTAAAG 599
Db |||||
Qy 4019 GAAGTATTTTCAACATATTACTTCTCTCTATCATATTTTATGAGGTATAGCTGAA 3960
Qy 600 AAAAGCAATTTTCCGGAATTTTCATGAGATCATATTTTGGAGCGCTCGGACAAATG 659
Db |||||
Qy 3959 AGGAGACATTTTTCGAAATCTTGGGTCTATCTAGCATACGCTTTTCTTGGAAACAGCA 3900
Qy 660 ATATCTCTTTTCACAATATCTATTGCTGCCATTCGAATATTCAGCAGATGAACATTTGA 719
Db |||||
Qy 3899 ATTTCTTTTCTGTTATGGTCAATATGCTGTATGCTGTATGAGGTAAAGTAAAG 3840
Qy 720 ACGTGGATGTAGAGATTTT-----CTTGCAATTTGGAGCCATCTTTTCT 764
Db |||||
Qy 3839 GGACAACTTCAGGAGATTTTACTTTTACAGATTGCTCTACTGTTTGGTGCATTTATCA 3780
Qy 765 GCGACAGATTTCTGCTGCAATTCAGGTCTCTAATCAGATGAGACACCTTT---TTG 821
Db |||||

Db 3779 GCAACTGATCCAGTACGCTGTTCTTGCTATATATCCAGAGCTTCAAGTGTGATGTTGAACATC 3720
Qy 822 TACAGTCTGGTATTCGGTGAAGGTGTGTGAACGATGCTACATCAATTTGCTGCTTTTCAAC 881
Db 3719 TATGCACTTCTTTTGTGGAAGGTCTCTCAATGATGCTGTTCCTGATGCTGCTCTCC 3660
Qy 882 GCACTACAGAACTTTGATCTTG-----TCACATAGATGGGCTGCTGCTT 926
Db 3659 TCAATAGTGGCATACCAAGCCAGCTGGAGACAACAGTCAACACCTTTGATGTCACAGCGATG 3600
Qy 927 CTGAAATCTTGGGAACCTCTTTTATTTATTTTGTGCGAGCACCTTCCCTGGAGTATTT 986
Db 3599 TTCAAGTCTATTTGGGATCTTCTCTTGGAACTCTTCAGTGGATCTTTGCAATGGGTGCTGCT 3540
Qy 987 GCTGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTTGAAGGCACTTCTACTGAC 1046
Db 3539 ACTGGAGTGGTACAGCTT---TAGTGACAAAGTTTACCAAAATACGGGAGTTCCAGTTG 3483
Qy 1047 CGTGAAGTGGCTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCTGAGTTGCTA 1106
Db 3482 TTGGAGACAGGCTGTTCTTCTTCTGATGCTCCTGGAGTACCTTCTCTTGGCTGAAGCATGG 3423
Qy 1107 GATTTGAGCGCACTTCCAGGATTTCTCTGTTGTTATGTTGATGTCACATTTACATTTGG 1166
Db 3422 GGCTTCAAGGTGATGTTGCGATATTTGTTGGCATCACAAAGCACATTTATACGTAT 3363
Qy 1167 CATAACGTCACAGAGTTCAAGAGTTTACAAACAAAGCAGCATTTGCAACTCTGTCCTTC 1226
Db 3362 AATAATTTGTCACGGAGTCTCAGCATAGAACTAAACAGTTGTTGAGCTTCTCAATTTTC 3303
Qy 1227 ATTCTGAGACTTTTCTCTCTGCTATGTTGGGATG 1262
Db 3302 TTGGCAGAGAAATTCATCTTCTCTCATACATGGGCTG 3267

RESULT 9

US-09-800-729-58
; Sequence 58, Application US/09800729
; Patent No. US2002068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 1354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-58

Query Match 2.2%; Score 52.4; DB 10; Length 1354;
Best Local Similarity 52.8%; Pred. No. 2.2e-05;
Matches 113; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 1050 GAGGTTGCCCTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCTGAGTTGCTAGAT 1109
Db 18 GAGACGGGCTGTTCTTCTCTCATGCTCCTGGAGCAGTTCTCTTGGCAGAGCCCTGGGA 77
Qy 1110 TTGAGCGGCATCTTCAACGATTTCTTCTGCTGATTTGTAATGTCACATTTACATTTGGCAT 1169
Db 78 TTTACAGGTGTTGATGCTGCTCTTCTGTTGGAATTCACAAAGCTCATTTACACCTACAAC 137
Qy 1170 AACGTCACAGAGTTCAAGAGTTTACAAAGCAGCATTTGCAACTCTGCTCTTCATT 1229
Db 138 AATCTGTGGTGAATCAAGAAGTCGAACCAAGCAGCTCTTTGAGGTGTACATTTCTCTG 197

Qy 1230 GCTGAGACTTTTCTCTTCTCTGATGTTGGGATGG 1263
Db 198 GCAGAGAACTTCTCTCTCTCATATGGCCTGG 231

RESULT 10

US-10-217-096-3
; Sequence 3, Application US/10217096
; Publication No. US2003004493A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J., Ferriera, Holly M.
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
; FILE REFERENCE: MP101-147PIRM
; CURRENT APPLICATION NUMBER: US/10/217,096
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1935)
US-10-217-096-3

Query Match 2.2%; Score 51.4; DB 9; Length 1935;

Best Local Similarity 46.2%; Pred. No. 5.9e-05;
Matches 350; Conservative 0; Mismatches 371; Indels 36; Gaps 4;

Qy 540 GATCTCTTCTTCTCATCTACCTCCTCCTCCGATCATCTTCAATGCAAGTTCAGGTAAAG 599
Db 394 GAAATCTTCTTCAATGTTTACTGCCACCAATATATTTTCATGAGGATATAGTCTAAAG 453
Qy 600 AAAAAAGCAATTTCCGGAATTTATGACGATCACATTTATTTGGAGCCGCGGCAATG 659
Db 454 AAGAGACACTTTTTCAAAACCTTAGGATCTATTTTAAAGTATGCTCTTCTGGGAAGTCC 513
Qy 660 ATATCTCTTTTTCACATA-----TCTATGCTGCCATTCATATATTC 701
Db 514 ATCTCTCTGATCGTCAATGGGTTAATGATGTTTGTGAAGGCTATGATCATGCT 573
Qy 702 AGCAGAAATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTCAATTTGGAGCCATCTTT 761
Db 574 GGCCAGCTGAAAATGGAGACTTTTCACTGATGTTTATTTTGTGTTCACTGATG 633
Qy 762 TCTGCGACAGATTTCTGCTGCACTTTGCAAGTTCCTCAAT---CAGGATGAGACACCTTTT 818
Db 634 TCTGCTACAGATCCAGTGCAGTGCCTGGCCATTTTCCATGAACCTGCACTGCACTGAC 693
Qy 819 TTGTACAGTCTGTTATTCGGTGAAGGTGTTGGAAGGATGCTACATCAATTTGCTGTTTC 878
Db 694 CTGTACACACTCTTGTGTTGGAGAGATGTTGTAATGATGCTGAGTGGCCATGCTCTTACA 753
Qy 879 AAGCACTACAGAACTTTTGTATCTTGTCCACA-----TAGATCGGCTGCTGCTT 926
Db 754 TATCTATATCTTATTTACAGTCCCAAGGAGATCCAAATGCAATTTGATGCGCAGCATTC 813
Qy 927 CTGAAATCTTGGGAACCTCTTTTATTTATTTTGTGAGACACCTTCTTCTGGAGATTTT 986
Db 814 TTCCAGTCTGTGGGAAATTTCTCT---GGGAATCTTCTGCTGGCTCATTTGCAATGGGCTCT 870
Qy 987 GCTGGATGCTCAGTGCATACATAATCAAGAAGCTATACATTTGGAAGGCAATTTCTACTGAC 1046
Db 871 GCGTATGCGCATCATCACAGCACTGTTGACCAAAATTTACCAAGCTGTGTGAGTTCGCGATG 930
Qy 1047 CGTGAAGTTGCCCTTATGATGCTCATGCTTACCTTTTATATATGCTGCTGAGTTGCTA 1106
Db 931 CTGAAACCGGCTGTTTCTTCTGCTTCTTGGAGTGCCTTCTGCTGCGGAGGCTGCC 990

QY 1107 GATTGAGGGCAATCTCCCGTATTTCTCTGTGTATTTGTAATGTCAATTACACTTGG 1166
Db 991 GGCCTAACAGGGATAGTTGCTCTTCTCTGTGTGAGTACACAAGCACATTTATACCTAC 1050
QY 1167 CATACAGTCACAGAGATTCAAGAGTTACAACAAGACGCAATTTGCAACTCTGCTTTC 1226
Db 1051 AACATCTGTCTTCGGATTTCCAAAATAGAACTAAACAGTTGTTTGAATTTATGAACATTT 1110
QY 1227 ATTGCTGAGACTTTTCTCTCTGCTATGTTGGATGG 1263
Db 1111 TTGGCGGAGAGCTCATCTCTGTATACATGGCCTGG 1147
RESULT 11
US-10-217-096-1
; Sequence 1, Application US/10217096
; Publication No. US20030044933A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J., Ferriera, Holly M.
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
; FILE REFERENCE: MPI01-147P1RM
; CURRENT APPLICATION NUMBER: US/10/217,096
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/312,544
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(2016)
US-10-217-096-1

Query Match 2.2%; Score 51.4; DB 9; Length 3537;
Best Local Similarity 46.2%; Pred. No. 9.2e-05;
Matches 350; Conservative 0; Mismatches 371; Indels 36; Gaps 4;

QY 540 GATCTCTTCTCATCTACTCTCCCTCCGATCATCTTCAATGCAAGGTTTTCAGGTAAAG 599
Db 475 GAAATCTTCTCAAGTTTATCTGCGCAATATATTTTCAGGAGATATAGTCTAAAG 534
QY 600 AAAAGCAATTTCTCCGAAATTCATGACGATCATATTTTGGAGCGCTCGGACAAATG 659
Db 535 AAGACACATTTTTCAAAACCTTAGGATCTATTTTAAAGTATGCTTCTTGGAACTGCC 594
QY 660 ATATCTTTTTCACAATA-----TCTATGTGCTGCCAATTCGAATATTC 701
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QY 702 AGCAGATGAACATTGGAACTGATGAGATGTTTCTTGCATTTGGAGGCAATCTTT 761
Db 655 GGCCAGCTGAAAAATGGAGACTTTCAATTCATGACTGCTTTATTTTGTGTTCACTGATG 714
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QY 819 TTGTACAGTCTGGTATTCGGTGAAGGTTGTGTAACGATGTACATCAATTTGTGCTTTTC 878
Db 775 CTGTACACACTCTTGTGAGAGAGTGTGTAATGATGCAAGTGGCCATAGTCTCTTACA 834
QY 879 AACCACCTACAGAACTTTGATCTTGTCCACA-----TAGATGGGCTGTGCTT 926
Db 835 TATTCATATCCATTTACAGTCCCAAGAGAAATCCAAATGCAATTTGATGCGCGACATTC 894
QY 927 CTGAAATCTTTGGGAACTCTTTTATTTATTTTGTGCGACACCTTCTTGGAGTATTT 986
Db 895 TTCCAGTCTGTGGGAATTTTCT---GGGAATCTTCGCTGCTCATTTGCAATGGGCTCT 951

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Db 952 GCGTATGCCATCATCACAGCACTGTTGACCAAAATTTACCAAGCTGTGTGAGTTCCCGATG 1011
QY 1047 CGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTTACATATATGCTGGCTGAGTTGCTA 1106
Db 1012 CTGAAAACCGGCTGTTTTCCTGCTTTCTTTGGAGTGGCTTCTCTGCGGAGCTGCC 1071
QY 1107 GATTGAGCGGCAATCTCACCGTATTTCTCTGTGTGATTTGTAATGTCAATTACACTTGG 1166
Db 1072 GGCCTAACAGGATAGTTGCTGTTCTCTCTGTGAGTACACAAGCACATTTATACCTAC 1131
QY 1167 CATAACGTCACAGAGATTCAAGAGTTACAACAAGACGCAATTTGCAACTCTGCTTTC 1226
Db 1132 AACAACTGTCTTCGGATTTCCAAAATAAGAACTAAACAGTTGTTTGAATTTATGAACATTT 1191
QY 1227 ATTGCTGAGACTTTTCTCTCTGCTATGTTGGATGG 1263
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RESULT 12

US-09-815-242-7730
; Sequence 7730, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7730
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1305)
US-09-815-242-7730

Query Match 1.9%; Score 44.4; DB 10; Length 1305;
Best Local Similarity 46.2%; Pred. No. 0.0069;
Matches 147; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 299 GGGGATGGAGTGGCGGCGGCGGCTTGTACACGACCTCCGACTACGGCTC 358
Db 726 GGTCAAGAGCTGTTCCTCCGAGCGCAGCGGTACTCTGACGCTTACGACCAACGCGCT 785
QY 359 GGTGGTGTCCATCAACCTGTTGCTGCGCTGCTGTGCGCTGATGCTCTCGGCCACCT 418

Db 786 GCTCGGCGCGCTCGGTGTTGGCCCATGCTGTCACCTGCGGCGGAATGCCAGCG 845
Qy 419 CCTGAGGAGATCGCTGGGTCAATGATCCATCACCGCGCTCATCATCGGGCTCTGCAC 478
Db 846 CTTGGCGGAGACTGCTGCGCGGTGGGTCTTCCCGACCTCCAACCTGTTCTCTCGGCAG 905
Qy 479 CGGCGTGTGATCTGCTGATGACCAAGGAGAGAGCTCGCACTTATTCGTTCTTCAGTGA 538
Db 906 CGGTCTGTTGACCTGCGAGCTGGAGCGCTACAAGGTCAAGTTCGGCTTCGGCACCGA 965
Qy 539 GGATCTCTTCTTCACTACCTCTCCCTCCGATCACTTCAATGACGAGTTTTCAGGTAAA 598
Db 966 TGTGCGGCGCGGACCACTGCTTCCAGCTGCTCCAGCTGCTGAGCGGCTGACAGGTTCAT 1025
Qy 599 GAAAAAGCAATTTCTCCG 616
Db 1026 GCAATTGAGGGCGCGG 1043

RESULT 13

US-10-033-109-9

; Sequence 9, Application US/10033109

; Patent No. US20020142390A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafaleki, J. Antoni

; APPLICANT: Sakai, Hajime

; TITLE OF INVENTION: Nitrogen Transport Metabolism

; FILE REFERENCE: BB-1210

; CURRENT APPLICATION NUMBER: US/10/033,109

; PRIOR FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248

; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 9

; LENGTH: 1883

; TYPE: DNA

; ORGANISM: Oryza sativa

US-10-033-109-9

Query Match 1.8%; Score 43.4; DB 12; Length 1883;
Best Local Similarity 47.3%; Pred. No. 0.019;
Matches 131; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Db 524 CACGCTGGTGTCTGCTCGCGGGTCTCTCTCGGGAGGATGAACATCAAGGGTGGATGGC 583
Qy 356 GTCGGTGTGTTCATCAACCTGTTGTCGCGCTGCTGCGCGCTGCAATGCTCTCTCGGCCA 415
Db 584 GTTCACTCGCTCTGGCTCTCTTCTCTACACCGCTGTCGCGCTTCAGCCTCTGGGGCGG 643
Qy 416 CCTCTCGAGGAGATCGCTGGTCAATGAGTCCATCACCGCTCATCATCGGGCTCTG 475
Db 644 CGGCTTCTCTACCAAGTGGGGGCTCATGCTACTTCCGGGGATGATGATCACTCTC 703
Qy 476 CACCGCGTGTGTGATCTTGTGATGACCAAGGAGAGCTCGCACTTATTCGTTTCAG 535
Db 704 CTCGGGATCGCGGCTTTCACCGCGCTTCTGTTGGGGCGGAGGCTGAGAGCGACAG 763
Qy 536 TGAGGATCTTCTTTCATCTACCTCTCTCCCTCCGATC 572
Db 764 GGAGCGGTTCTCGCGGAACAACATCTCTCTCATGATC 800

RESULT 14

US-09-887-576-816

; Sequence 816, Application US/09887576

; Patent No. US20020144047A1

; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 816
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-576-816

Query Match 1.8%; Score 43; DB 10; Length 690;

Best Local Similarity 49.3%; Pred. No. 0.012;

Matches 112; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 262 CGTGTGGTGGCGGAGAAAGTCCCGCTGAGGATGGGATGGAGTGGCGGCGGC 321
Db 71 CGCTGGCGGCTCTGCTGGGTGGTGGCGCTTGGCGCAACGCGCTGGCGCGCGGG 130
Qy 322 GCGTGGGGCTCTGTACAGCACTCGGACTAGCGCTCGTGTGTCCATCAACCTGTCG 381
Db 131 TGGCGGTTTTCGCGCAACGCTTCGGCGGCGCACTCAACCGGCGCTCAGTTCCGGCTGC 190
Qy 382 TCGCGCTGCTGCGCGCTGCATGCTCGGCGCACTCTCTCGAGGAGAATCGCTGGGTCA 441
Db 191 TGTGCGGCGCGCATCTCTTCTCGCGCGCGCGCTCTACTGGGCGGCCAGCTGCTCG 250
Qy 442 ATGAGTCCATCACCGCGCTCATCATCGGGCTCTGACCGGCGTGTG 488
Db 251 GCGCGGTGCTGCGCGTGTCTTCTCTCCTCAGGCTGGCTCCGAGGCGCATG 297

RESULT 15

US-10-040-739-929

; Sequence 929, Application US/10040739

; Patent No. US20020173635A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John

; LaVallie, Edward

; Racie, Lisa

; Merberg, David

; Treacy, Maurice

; Spaulding, Vikki

; TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS

; NUMBER OF SEQUENCES: 1519

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 12:22:03 ; Search time 3711 Seconds
(without alignments)
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Title: US-09-888-035A-1

Perfect score: 2330

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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	745.8	32.0	3272	11 AY109416	AY109416 Zea mays
3	656.8	28.2	711	9 AU094795	AU094795 AU094795
4	566	24.3	719	13 BJ312595	BJ312595 BJ312595
5	473.2	20.3	1212	10 BE420587	BE420587 HWM000.D1
6	412.2	17.7	690	14 BQ865196	BQ865196 QGC2a03.Y

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15	340.4	14.6	378	14 C91832	C91832 C91832 Rice
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39	218.6	9.4	556	10 BE600656	BE600656 PII_91_A1
40	218.2	9.4	565	14 BQ163719	BQ163719 952081B08
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43	210.2	9.0	401	10 BE607262	BE607262 NXCI_034
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ALIGNMENTS

RESULT 1
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LOCUS AY105332 2080 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0131050 mRNA sequence.
ACCESSION AY105332
VERSION AY105332.1 GI:21208410
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE 1 (bases 1 to 2080)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2080)
AUTHORS Coe,E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public configs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 483 a 505 c 471 g 621 t

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Best Local Similarity 69.9%; Pred. NO. 3e-164;
Matches 1130; Conservative 0; Mismatches 486; Indels 1; Gaps 1;

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DB 403 AACTCACGCACTTCTGTGTTGAGCGAGACCTGTTTTCATATATTTACTTCCGCGGATA 462
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DB 1723 GGTGTTTCGGGGGGGAGGTTTTCGTCTCTTGTGCTCTTGTGCTGCTGGTGGAGAGGAG 1779
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RESULT 2

LOCUS AY109416 Zea mays CL694_1 mRNA 3272 bp linear HTC 25-MAY-2002
DEFINITION Zea mays CL694_1 mRNA sequence.
ACCESSION AY109416
VERSION AY109416.1 GI:21213132
KEYWORDS HTC.

SOURCE

ORGANISM Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3272)

REFERENCE

AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes

JOURNAL

REFERENCE 2 (bases 1 to 3272)
Unpublished (2002)

AUTHORS

Coe, E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

FEATURES

source

Location/Qualifiers
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 /lib="Maize Mapping Project/DuPont Cornsensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 652 a 745 c 726 g 812 t 337 others
 ORIGIN

Query Match 32.0%; Score 745.8; DB 11; Length 3272;
 Best Local Similarity 67.5%; Pred. No. 4e-147;
 Matches 1079; Conservative 0; Mismatches 497; Indels 22; Gaps 4;

QY 313 CGGCGCGCGCTGGGCTCTGTACAGCACTCCGACTAGCGCTCGGTGGTGCATCA 372
 DB 53 CTGGATGGCGCTGGCGTGGGACCGCGCAGCGACTAGCCTCCATCGCGCGGTGG 112
 QY 373 ACCTGTTCTGTCGCGCTGCTCGCGCTGCTCGCTCGGCACTCTCTCGAGGAAATC 432
 DB 113 GGCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGCACTCTCTCGAGGAAAC 172
 QY 433 GCTGGTCAATGAGTCCATCAACCGGCTCATCTCGGCTCTGCAACCGCGGTGGTATCT 492
 DB 173 GCTGGATGAACGAGTCCATCAACCGGCTCTCTCATCGGCTGGGAACTGGAGCGGTCTATCC 232
 QY 493 TGCTGATGACCAAGGAGAGCTCGCACTTATTCGTCTCAGTGAGGATCTCTCTTCA 552
 DB 233 TGTTCGCTGAGCGGGAAGCAITTCGCGCGTGGTGTTCAGGAGGACCTCTCTTTTA 292
 QY 553 TCTACCTCCTCCCTCCGATCATCTTCAATGAGGTTTTTCAGGTAAAGAAAAGCAATCT 612
 DB 293 TTTACCTGCTCGCGGATCATATTCATGAGGTTTCCAAGTGAAGAAAGCAATCTCT 352
 QY 613 TCCGGAATTCATGAGATCAATATTTGAGCGCTCGGACAAATGATATCTTTTTCA 672
 DB 353 TTCGAAATCTCATTAATTAATCACTGTTTGGTGCAGTTGGCACTGATCTCTTTACTG 412
 QY 673 CAATATCTATTCGTCGCAATTCGAATATTCAGCAGAAATGGAACCTGGATGATAG 732
 DB 413 TAATATCCCTTGGCGCTCTAGGACTAATATCAAGGCTTAAATATCGGCGCACTTGAATCG 472
 QY 733 GAGATTTTCTTGCAATTCGAGCCATCTTTCTGCGACAGATTCGTCTGCACATTCGAGG 792
 DB 473 GAGACTATCTTGCACTTGGGCAATATTCGCGCAAGACTCGGTTGCACTTGGAGG 532
 QY 793 TCCTCAATCAGAGTGAACAACCTTTTGTACAGTCTGGTATTCGGTGAAGGTTGTGA 852
 DB 533 TGTTAAGCAAGATGAGACCAATCTTGTACAGCTCGTGTGGTGAAGTGTGTCA 592
 QY 853 ACGATGCTACATCAATTCGTCTTTCAGCGCACTACAGAACTTGAATCTGTCCACATAG 912
 DB 593 ATGAGCAACTCTGTGTGTGTTCATATGCAATCCAGAACTTGAATCTGTGAAATATCA 652
 QY 913 ATGCGGCTGTGCTGTAATCTTGGGAACTCTTTTATTTATTTTGTGCGAGCACT 972
 DB 653 GCAGTGCCAAATTAAGCACTTCAATGCGAGTTCCTTTATCTGTTCGGCTCCAGCACTA 712
 QY 973 TCCTTGGAGTATTCGTCGATTCGTCAGTGATACATATCAAGAACTATACATTCGAA 1032
 DB 713 TCTTTGGAGTAGTCTCTGCACTCTTAGTGTATACCATTAAGAAAGTTGTACTTCGCA 772
 QY 1033 GCAATCTACTGACCGTGGAGTTGCCCTTATGATGCTCATGGCTTACCTTTTATATATGC 1092
 DB 773 GGCATTCAACCGATCGTGAAGTTTCCATATGATGCTAATGGCTTATTTATCTTACATGC 832

QY 1093 TGGCTGAGTGTCTAGATTGAGCGGCAATCTCACCGTATTTCTTCTGTGTATTGTAATGT 1152
 DB 833 TAGTCAATTTGCTCGAATTTGAGTGGCAATCTCACCTGTGNNNNNCTGCGGTATCGTAATGT 892
 QY 1153 CACATTACATTTGGCATACCGTCAAGAGAGTTTCAAGAGTTTACAAAGACGCAATTTG 1212
 DB 893 CACACTATACITTTGGCACAATGTAAAGAAAGTTTCAGAGGTCAACCAAGCATGCTTTG 952
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 DB 953 CAACTGTCTGTTTATCTCCGAGACTTTTCTGTTTCTTTAT-TCGGTATGATGCAATGG 1011
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 QY 1327 GCTCAATTTTGTAGATTGTTCTGATTGGAGAGCTGCTTTTCTATTTCGCGTGTGCT 1386
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 QY 1447 TAATATGTTGGCTGGCTGATGAGAGAGCTGTGTGATTTGCTCTTGTCTTACAATAAGT 1506
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 QY 1567 CTGTGCTCTTTTATAGCACTATGTTGATTTGGATGATCAAAAGCAATGATGACGCTGC 1626
 DB 1312 GCGTGTCTTTTTCAGCAATGTTGTTGGCTGCTGACGAGGCCCTGATCAGGCTCT 1371
 QY 1627 TGCTACCG-----GCCTCAGGCACTCTGTCTCCTCTCAGGCTTTCATCACCAA 1674
 DB 1372 TGATCCCGTCAAGGCACTATCCAGGAAACCAAGCGCCCTTTCTGAACCTTCCAGCCGA 1431
 QY 1675 AGTCCCTGATTTCTCTCTCTGACAGCATGCAAG-----TTCTGACCTCGAGATACAA 1731
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 QY 1732 CAAACATTTGAGGCTTCCAGCTCCGATGCTCTCTCAACCAAGCGCACACACTGTCC 1791
 DB 1492 TAAGCTACGACCGCGGAGCTTCCGTTTCTCTAGTAGAGCGGCAACGGTCCGTCC 1551
 QY 1792 ACTACTTCTGGCGCAAGTTTCGACGCGCTGATGCGACCGATGTTTGGCGGCGCGGT 1851
 DB 1552 ACCATTACTGGCGCAAGTTTCGATGACAGTTTCATGCGGCGGTGTTGGTGGCGGTGGCT 1611
 QY 1852 TGTGTCCTTCTCCCTGATCACCACCGAGCAGAGC 1889
 DB 1612 TCGTCCCTTCTGCTGCTGTTTCAACCACTGAGAGCAGC 1649

RESULT 3

AU094795

LOCUS

DEFINITION

AU094795

ACCESSION

AU094795.1

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AU094795 711 bp mRNA linear EST 03-APR-2002
 AU094795 Rice panicle shorter than 3cm Oryza sativa (japonica
 cultivar-group) cDNA clone E31686, mRNA sequence.

GI:8857477

EST.

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 711)

Sasaki, T. and Yamamoto, K.

```

TITLE      Rice cDNA from panicle (2000)
JOURNAL    Unpublished (2000)
COMMENT    Contact: Takuji Sasaki
           National Institute of Agrobiological Resources
           Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
           305-8602, Japan
           Tel: 81-298-38-7441
           Fax: 81-298-38-7468
           Email: teasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
           PROJECT = 'RGP'.

FEATURES   Location/Qualifiers
            source
            1..711
            /organism="Oryza sativa (japonica cultivar-group)"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /clone="E31686"
            /clone_lib="Rice panicle shorter than 3cm"
            /dev_stage="shorter than 3cm"
            /note="Organ: panicle"

BASE COUNT 192 a 159 c 172 g 187 t 1 others
ORIGIN
Query Match      28.2%; Score 656.8; DB 9; Length 711;
Best Local Similarity 99.4%; Pred. No. 3.8e-128;
Matches 669; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1648 CTGTCACCTCTGAGCCTTCATCACCAAGTCCCTGCATTCT-CCTCTCTGCACAGCATG 1706
      |||
Db 1 CTNTCACCTCTGAGCCTTCATCACCAAGTCCCTGCATTCTCCCTCTCTGACAGCATG 60

Qy 1707 CAAGTTCTGACCTCGAGAGTACACCAACATGTGAGCGCTTCAGCCTCCGGATGCTC 1766
      |||
Db 61 CAAGTTCTGACCTCGAGAGTACACCAACATGTGAGCGCTTCAGCCTCCGGATGCTC 120

Qy 1767 CTCACCAAGCCGACCACTGTCACACTACTGCGCCAGATTCGACGCGCGCTGATG 1826
      |||
Db 121 CTCACCAAGCCGACCACTGTCACACTACTGCGCCAGATTCGACGCGCGCTGATG 180

Qy 1827 CGACCGATGTTTGGCGGCGCGGTTGCTGCCCTTCTCCCTGGATCACCAACCGAGCAG 1886
      |||
Db 181 CGACCGATGTTTGGCGGCGCGGTTGCTGCCCTTCTCCCTGGATCACCAACCGAGCAG 240

Qy 1887 AGCCATGAGGAAGTGAACAGTCAACAGAAATGAGATGGAATGGTTGATGAGGAGAT 1946
      |||
Db 241 AGCCATGAGGAAGTGAACAGTCAACAGAAATGAGATGGAATGGTTGATGAGGAGAT 300

Qy 1947 ACATGTAATAATGTGACACAAAGAGAGAGCAAGTGTTCGGTTTGTAGAGTTTGGCTG 2006
      |||
Db 301 ACATGTAATAATGTGACACAAAGAGAGAGCAAGTGTTCGGTTTGTAGAGTTTGGCTG 360

Qy 2007 CTGCTAATGAGTTGTGATAGTGCCCTATATTTCTTCAGAACTTCAGATGGTGCTCACCAA 2066
      |||
Db 361 CTGCTAATGAGTTGTGATAGTGCCCTATATTTCTTCAGAACTTCAGATGGTGCTCACCAA 420

Qy 2067 GGCCTAAGAGCCAGGAGACCTTCTGATAATGGTTTCGGGATGATGGTTTGTCTGTGAG 2126
      |||
Db 421 GGCCTAAGAGCCAGGAGACCTTCTGATAATGGTTTCGGGATGATGGTTTGTCTGTGAG 480

Qy 2127 GATGAACCTTAGTGATGACACAGGTCATGTGCTCCGACACCTGTAAATTTGTAGAT 2186
      |||
Db 481 GATGAACCTTAGTGATGACACAGGTCATGTGCTCCGACACCTGTAAATTTGTAGAT 540

Qy 2187 TAACAGCCCCATTTGTACCTGTACCACTTTTGTAGTTGGCGGGTGTCTTTCCCTAGTTGC 2246
      |||
Db 541 TAACAGCCCCATTTGTACCTGTACCACTTTTGTAGTTGGCGGGTGTCTTTCCCTAGTTGC 600

Qy 2247 CACCTGATGATAAATGAAATTCCTCCGCCAAATAGATTTGTGTGATATAAATTTTGC 2306
      |||
Db 601 CACCTGATGATAAATGAAATTCCTCCGCCAAATAGATTTGTGTGATATAAATTTTGC 660

Qy 2307 TTGGTTGAAAAA 2319
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Db 661 TTGGTTGATAAA 673
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RESULT 4
BJ312595
LOCUS    BJ312595      719 bp      mRNA      linear      EST 09-APR-2002
DEFINITION
BJ312595 Y. Ogiwara unpublished cDNA library, Wh_yf Triticum
aestivum cDNA clone whylf10p07 5', mRNA sequence.
ACCESSION
BJ312595
VERSION  BJ312595.1 GI:20119380
KEYWORDS EST.
SOURCE    bread wheat.
          Triticum aestivum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
          ; Triticeae; Triticum.
          1 (bases 1 to 719)
AUTHORS   Ogiwara,Y. and Murai,K.
TITLE      Expressed genes in Triticum aestivum
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-i
          National Institute of Genetics
          Center For Genetic Resource Information
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
          Email: tshini@genes.nig.ac.jp.
          Location/Qualifiers
            1..719
            /organism="Triticum aestivum"
            /cultivar="Chinese Spring"
            /db_xref="taxon:4565"
            /clone="whyf10p07"
            /clone_lib="Y. Ogiwara unpublished cDNA library, Wh_yf"
            /tissue_type="spikelet at early flowering"
            /dev_stage="Peekes' scale 6"
            /note="Vector: lambda Uni-ZAP XR, excised phagemid;
            Site 1: EcoRI; Site 2: XhoI; Plants were grown under
            hydroponic conditions at UC Davis, salt stressed for 12
            hours, and for 7 days, then dissected and frozen (Akhunov
            in J Dvorak Lab). Total RNA was prepared from sheath
            tissue, equal quantities of RNA were pooled from the two
            samples, polyA was purified from the pooled RNA, a cDNA
            library was made, and the cDNA clones were in vivo
            excised to give pBluescript phagemids in the TJ Clonase lab
            at the University of California, Riverside (Akhunov, Chin
            , Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
            Plasmid DNA preparations and DNA sequencing were
            performed in the OD Anderson lab (all other authors)."
```

BASE COUNT 168 a 154 c 178 g 218 t 1 others

ORIGIN

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Query Match      24.3%; Score 566; DB 13; Length 719;
Best Local Similarity 87.9%; Pred. No. 5e-109;
Matches 617; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 809 GACACCCCTTTTGTACAGTCTGGTATTTCGGTGAAGGTGTTGTGAACGATGTCATCAAT 868
      |||
Db 18 GAGGCCCTTTTGTACAGTCTAGTGTTCGGGGAAGGTGTTGTGAACGATGCCACATCGGT 77

Qy 869 TGTGCTTTTCAACGCACCTACAGAACTTTGATCTTGTCCACATAGATCGGCTGCTGTTCT 928
      |||
Db 78 CGTGCTTTTCAACGCCTCCAGAACTTCGATCCTTAACAGATCGACGATCGTCATTTCT 137

Qy 929 GAAATCTTCGGGAACCTCTTTTATTTTATTTTGTCTGAGCACCTTCTCTGGAGTATTGC 988
      |||
Db 138 TAAGTTCTTCGGGAACCTCTCTGCTACTTATTCGTTGTCAGACCTTCTCTGGAGTATTGC 197

Qy 989 TGGATTGCTCAGTGATACATAAATCAAGAAGCTATACATTGGAAGGCAATCTACTGACCG 1048
      |||
Db 198 TGGATTGCTTAGTGATACGTATCAAGAAATATACATAGGAAGGCAATCTACTGACCG 257

Qy 1049 TGAGTTGCCCTTATGATGCTCATGGCTTACCTTTCATATATGCTGCTGAGTTGCTAGA 1108
      |||
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Db 258 TGAGTGCACCTGTGTGATGCTATGGGCTACCTCTCATATATGCTAGCTGAGCTGTGAGA 317

Qy 1109 TTTGAGCGGCAATCTTCACCGTATTTCTTCTGTGGTATTTGTAATGTACATATACATTCAGCA 1168

Db 318 TTTGAGTGGTATCTCTCACTGTATTTCTTCTGTGGTATTTGTAATGTACATATACATTCAGCA 377

Qy 1169 TAAAGTACAGAGAGTTCAGAGATTACAAAGACGCAATTTGCAACTCTGTCTTCAT 1228

Db 378 TAAAGTACAGAGAGTTCAGAGATTACAAAGACGCAATTTGCAACTCTGTCTTCAT 437

Qy 1229 TGCTGAGACTTTCTTCTTCCTGTATTTGGGATGGATGCAATTTGCAACTCTGTCTTCAT 1288

Db 438 TGCCGAGACTTTCTTCTTCCTTTATTTGGGATGGATGCAATTTGCAACTCTGTCTTCAT 497

Qy 1289 GTTTGCCAGTACAGACCTGGCAATCCATTGGGATAGCTCAATTTTGTAGGATTTGGT 1348

Db 498 ATTTGCTAGTACAGACCTGGCAATCCATTGGGATAGCTCAATTTTGTAGGATTTGGT 557

Qy 1349 TCTGATTTGGAAGAGTGTCTTTGTTATTTCCCGCTGTCTTTCTGTGCAACCTTACAAAGAA 1408

Db 558 TCTGTTGGAAGAGTGTCTTTGTTATTTCCCGCTGTCTTTCTGTGCAACCTTACAAAGAA 617

Qy 1409 GGCACCGAATGAAATAAACCCTGGAGACAGCAATTTGTAATATGTTGGTGGCTGTAT 1468

Db 618 GACGAGCTTGAAATAAACCCTGGAGACAGCAATTTGTAATATGTTGGTGGCTGTAT 677

Qy 1469 GAGAGGAGCTGTGTGATTTGCTTTGCTTACAAATAGTTTAC 1510

Db 678 GAGAGGAGCTGTGTGATTTGCTTTGCTTACAAATAGTTTAC 719

RESULT 5

BE420587 1212 bp mRNA linear EST 24-JUL-2000

LOCUS HM000.D12 ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone

DEFINITION HM000.D12, mRNA sequence.

ACCESSION BE420587

VERSION BE420587.1 GI:9418430

KEYWORDS EST.

SOURCE Hordeum vulgare.

ORGANISM Hordeum vulgare.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum.

AUTHORS 1 (bases 1 to 1212)

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudriet, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.

TITLE International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

JOURNAL Unpublished (2000)

COMMENT Contact: Herrmann RG

Botanisches Institut der LMU

Menzinger Str. 67, D-80638 Munchen GERMANY

Fax: 49 30 171683

Email: hermann@botanik.biologie.uni-muenchen.de

International Triticeae EST Cooperative (ITEC)

http://wheat.pw.usda.gov/genome.

Location/Qualifiers

1. 1212

/organism="Hordeum vulgare"

/cultivar="Barke"

/db_xref="taxon:4513"

/clone="HM000.D12"

/clone.lib="ITEC HWM Barley Leaf Library"

/tissue type="leaf"

/dev stage="14 day old"

/note="Vector: pBluescriptSK(-); 850 bp average insert size."

BASE COUNT 296 a 294 c 276 g 346 t

ORIGIN

Query Match 20.3%; Score 473.2; DB 10; Length 1212;

Best Local Similarity 73.0%; Pred. No. 1.5e-89;

Matches 651; Conservative 0; Mismatches 233; Indels 8; Gaps 3;

Qy 600 AAAAAGCAATTTCTTCGGNAATTTTCATGAGCATCACATTTATTTGGAGCGCTCGGGCAATG 659

Db 57 AGAGAACAAATTTCTTCGGCAATTTTCATGACTATTACATTTGTTTGGCGTATTTGGGACCTTG 116

Qy 660 ATATCTCTTTTTCACAAATATCTATCTGTCATTTGCAATTTTTCAGCAGAAATGAACATGGA 719

Db 117 ATCTCTCTTCAGTATATATCATCTTGTGTCATTTGGGCTAGTATCAAGGCTGAACATAGGC 176

Qy 720 AGCTGGATGTAGGAGATTTTCTTGCAATTTGGAGCAATTTTCTTGCGACAGATTTCTGTC 779

Db 177 GCGCTTGAGCTTTGGAGACTTACCTCGCACTTTGGGCAATATTCTCGGCAACGGACTCTCTT 236

Qy 780 TGCACATTTGCAGGTCTCAATCAGGATGAGACACCTTTTGTACAGTCTGCTATTCGGT 839

Db 237 CGCACCTTGCAGGTGTAAAGCCAAAGATGAGACACCTTTTCTTGATCAGTTTGGTGTGGT 296

Qy 840 GAAGGTGTTGTGAACGATGCTACATCAATTTGTGCTTTTCAACGCACTACAGAACTTTGAT 899

Db 297 GAAGGTGTTGTGAACGATGCTACATCAATTTGTGCTTTTCAACGCACTACAGAACTTTGAT 356

Qy 900 CTTGTCCACATAGATCGGCTGTCTGTTCTGAAATTTCTTGGGAACTTTCTTTTATTTATTT 959

Db 357 CTTGGAAATTTTCAGTAGCCTCAAAATTTCTTACAATTTCAATTTGGAATTTCTCTATCTATT 416

Qy 960 TTGTGAGACACCTTCTTGGAGTATTTGCTGATTTGCTCAGTGCATACATATCAAGAG 1019

Db 417 GCGCCAGTACCTTTCTTGGAGTATCTAGTGGACTTCTCAGTGCATATGTCATCAAGAAA 476

Qy 1020 CTATACATTTGGAAGGCAATTTCTGACCTGAGTTTGCCTTATGATGCTCATGCTTAC 1079

Db 477 CTGTACTTTGGCAGGCACTTCACTGATCTGTAAGTTGCTATTTATGATGCTCATGCTTAT 536

Qy 1080 CTTTCATATATGCTGGCTGAGTTGCTAGATTTGAGGGCAATTTCTCACCGTATTTCTTGT 1139

Db 537 TTATCTTACATGCTGGCTGAATTTGCTTGAATTTGAGTGGTATTTCTCAGGTTTTCTTCTGT 596

Qy 1140 GGTATTTGTAATGTACATTTACACTTTGGCAATGCTGACAGAGTTCAAGAGTTACAACA 1199

Db 597 GGTATTTGTAATGTGCACTATACCTGGCAATGTAACAGAGAGTTCCAGGCTCAACC 656

Qy 1200 AAGCAGCAATTTTGCAACTCTGCTCTTCAATTTGCTGAGACTTTTCTCTCTGATTTGGG 1259

Db 657 AAGCATGCTTTTCCACATTTGATTTCACTCTCTGAGAGCTTTTCTCTTCTCTATGTTGGC 716

Qy 1260 ATGGATGCAATTTGGAATAATGGGAGTTTGGCAGTG-----ACAGACTGGCAAT 1314

Db 717 ATGGATGCAATTTGGAATAATGGGAGTTTGGGAGTTTGGTGTGTAACATATAGCCCAAT 776

Qy 1315 CATTTGGGATAGCTCAATTTTGTAGGATTTGCTGATTTGTAAGAGAGTCTGTTTGTAT 1374

Db 777 CTATTTGCTTTGAGCTCCATTTATTTTGGCGTGTGTTGCTGTTTGAAGAGTGTCAATTTGTT 836

Qy 1375 TCCCGCTGTCTTCTTGTGCAACCTTAAAGAGAGCCAGCAATGAAAAAATAACCTGGA 1434

Db 837 TCCCTCTATCTATCTCTCC--AATTGACCAAAAAAACTCCAGGCGAGAGATCTCTGTTA 894

Qy 1435 GACAGCAAGTTGTAATATATGTTGGGCTGTGATGAGAGAGCTGTGTCAT 1486

Db 895 GGCAGCAAGTTATTTTGTGGGC-GGCTCATGAGAGGGCGGTGTCAAT 945

RESULT 6

LOCUS BQ865196

DEFINITION BQ865196

QGC2a03.yg abi QG ABCDI lettuce salinas Lactuca sativa cDNA clone

QGC2a03, mRNA sequence.

ACCESSION BQ865196

690 bp mRNA linear EST 14-AUG-2002

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VERSION B0865196.1 GI:22250661
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 690)
Kozik, A., Micheltore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Micheltore]
Department of Vegetable Crops, R.W.Micheltore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [micheltore@vegmail.ucdavis.edu]
Belongs to contig QG_CA_Contig6585, see http://cgdb.ucdavis.edu/
for details.
Plate: QGC2 row: a column: 03.
FEATURES
Location/Qualifiers
source
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/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGC2a03"
/lab_host="E.coli"
/notes="vector: pRCONASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QG_ABCDI lettuce salinas
TAG_TISSUE=chemical induction
TAG_SEQ=TTGTAGCCGG"

BASE COUNT 180 a 112 c 149 g 248 t 1 others
ORIGIN
Query Match 17.7%; Score 412.2; DB 14; Length 690;
Best Local Similarity 74.8%; Pred. No. 1.3e-76;
Matches 516; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Qy 694 GCTGCCATTGCAATTCAGCAGAAATGAACATTTGGAACGCTGGATGTAGGAGATTTCTT 743
Db 1 GGTGCTATAAATATTTCCAAAGGATGATGTTGGTACCCCTTGAGCTTGGAGACTTTCTT 60

Qy 744 GCAATTGAGCACTTTTCTGGACAGATCTGCTGCAGATTCGAGTCTCAATCAG 803
Db 61 GCAATTGAGCAATATTTTCAGCACCAATTCGGTTTCGACCTTTCGAGTGTGAATCAG 120

Qy 804 GATGAGACACCTTTTGTACAGTCTGGTATTCGGTGAAGTGTGTGTAACGATGCTACA 863
Db 121 GATCAGACACCTTTATATATAGTTTGGTGTGGTGAAGTGTGGTGAATGATGCCACA 180

Qy 864 TCAATTGCTTTTCAACGCACTACAGAACTTTGATCTTTGTCATAGATGCGGCTGTC 923
Db 181 TCAGTTGTCATCTTCAATGCGAGTTCAAAACCTTTCATCTCTCTCAAAATCACAACTGCTGT 240

Qy 924 GTTCTGAATTTCTGGGAACCTCTTTTATTTATTTTGTGCGACACCTTCTCTGGAGTA 983
Db 241 GCAATTCAACTGATGGAAATTTCTTTTATTTATTTATTCATCAAGACACACTTCTAGGAGCT 300

```

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Qy 984 TTTGCTGATTGCTCAGTGATACATATCAAGAGCTATATACATTGGAGGCAATCTTACT 1043
Db 301 GGAGCTGGGCTACTAAGTGCTTATATATAAGAGCTATATTTTGGAGGCAATCAACT 360

Qy 1044 GACCGTAGGTTGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTGGCTGAGTTG 1103
Db 361 GATAGAGAAAGTTGCTATAATGATACATAATGATGCTTATCTTTTCATACATGCTAGCTGAGTTA 420

Qy 1104 CTAGATTGAGCGGCATCTCCACCGTATCTCTCTGCTGATTTGTAATGCTACATTCACACT 1163
Db 421 TTCTATTGATGGGATCTCTCACGGTTTCTCTCTGGAATTGATGCTCTCATTTACACT 480

Qy 1164 TGGCAATACGTCACAGAGAGTTCAAGAGTTACAACAAGACGCGATTTGCAACTCTGTCC 1223
Db 481 TGGCAATATGTCACAGAGAAATCTCGAGTAACCTACCAAGCATACCTTTGCAACATTGTCA 540

Qy 1224 TTCAATTGCTGAGACTTTTCTCTCTCTGATGTTGGGATGGAATGATGATTTGAAAAA 1283
Db 541 TTTGCTGCTGAGTTATTTATCTTTTATGTCGAAATGGAATGCTTTAGATATTTGAAAAG 600

Qy 1284 TGGGAGTTTCCAGTGCAGACAGACCTGGCAATCCATTGGGATAAGCTCAATTTGCTAGGA 1343
Db 601 TGGAGATTGTTAAAGACAGCCCTGGGACTTCNGTTGAAGTGAAGTGAATTTTATTTGGA 660

Qy 1344 TTGCTTCTGATTGGAAGAGCTGCTTTTGTGA 1373
Db 661 TTGCTTTTAGTTGGAAGAGAGCCCTTTGTA 690

RESULT 7
BI933988 665 bp mRNA linear EST 18-OCT-2001
LOCUS EST553877 tomato flower, anthesis Lycopersicon esculentum cDNA
DEFINITION clone CTOD18B13 5' end, mRNA sequence.
ACCESSION BI933988
VERSION BI933988.1 GI:16248460
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 665)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Unterback, T., Van Aken, S., Ronning, C.M., Niemman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3
Location/Qualifiers
1..665
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOD18B13"
/clone_lib="tomato flower, anthesis"
/tissue_type="flower"
/dev_stage="anthesis"
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
BASE COUNT 156 a 140 c 144 g 225 t

```


ORIGIN

Query Match 17.2%; Score 400.6; DB 13; Length 665;
Best Local Similarity 75.3%; Pred. No. 3.5e-74;
Matches 499; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 746 AATTGGAGCCATCTTTCTGCGACAGATTCTGTCTGCACATTCGAGTCTCAATCAGGA 805
DB 1 AATTGGAGCAATATTTGCTGCCACAGATTCGCTGCACATTCGAGTCTCAATCAGGA 60
QY 806 TGACACACCCCTTTTGTACAGTCTGGTATTCGGTGAAGGTGTGTGACATCTACATC 865
DB 61 TGACACACCCCTCTTTTACAGTCTGTATTTGGAGAGAGATTTGTAATGATCTACATC 120
QY 866 AATTGTGCTTTTCAACGCACATACAGAACTTTGATCTTGTCCACATACATCGCGTGTGCT 925
DB 121 GGTGGTCTTTTCAATGCTATTCAAAGCTTGACCTTACAGCTTGAATCCAGTATAGC 180
QY 926 TCTGAAATCTTTGGGAACTTTCTTTTATTTATTTTGTGAGCACCTTCTTGGAGTATT 985
DB 181 CCTCAGTTTCTTGGCAACTTCTTCTATCTGTCTTCTGCTAGCACTTTTACTGGAGCAGG 240
QY 986 TGTGGAATGCTAGTCATACATTAATCAAGAGCTATATTTGGCAGGCACTTCTACTGA 1045
DB 241 AACTGGTCTTCTTAGTGTCTTACATTAATCAAGAGCTGTATTTTGGCAGGCACTCCACGA 300
QY 1046 CCGTGAGGTTCCCTTATGATGCTCATGGCTTACCTTTTATATATGCTGGCTGATGCT 1105
DB 301 TCGTGAGGTTCCCTTATGATGCTCATGGCTTATTTATATACATGCTGCCGAACTATT 360
QY 1106 AGATTTGAGCGGCATTTCTCCCGTATTTCTTGTGATTTGTATGTCACATTTACACTTG 1165
DB 361 CTATTTGAGTGGATTTCTACCGTATTTTCTGTGATTTGTGATGCTCTATTACACTTG 420
QY 1166 GCATAACGTCACAGAGAGTCAAGAGTTCAAGAGTTCAACAAAGACGCACTTTCGAACTTGTCTCT 1225
DB 421 GCACAAATGACCGAGAGTCAAGAGTCACTTACAAAGGCACACTTTTGCACACTTTGTCAAT 480
QY 1226 CATGCTGAGACTTTCTCTTCTGTATGTTGGATGATGATGATGATGATGATGATGATGATG 1285
DB 481 TCTTGCAGAGACTTTCTCTTCTGTATGTTGGATGATGATGATGATGATGATGATGATGATG 540
QY 1286 GGAGTTTGCAGAGTGCAGACCTGGCAATCAATTCGATAGCTCAATTTTGTAGGATT 1345
DB 541 GAAATTTGTTGTCAGACGCTGGATATCAATTTCCGCAAGTCGATCTGATGGGACT 600
QY 1346 GGTCTGATTTGGAAGAGCTGCTTTTGTATTTCCCGCTGTGCTTCTGTGCAACCTTAACAA 1405
DB 601 AATCTTGTGGGAGACCTGCTTTTGTGTTTTCATATATCATCTATATCACTTATCAATGAA 660
QY 1406 GAA 1408
DB 661 GAA 663

RESULT 8

BJ316128
LOCUS BJ316128 632 bp mRNA linear EST 09-APR-2002
DEFINITION BJ316128 Y. Ogiwara unpublished cDNA library, Wh_yf Triticum
aestivum cDNA clone whyf21k06 5', mRNA sequence.

ACCESSION

BJ316128

VERSION

BJ316128.1 GI:20121504

KEYWORDS

EST.

SOURCE

bread wheat.

ORGANISM

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 632)
Ogiwara, Y. and Murai, K.
Expressed genes in Triticum aestivum
TITLE
Unpublished (2002)
Contact: Tadasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

1. 632
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whyf21k06"
/tissue_type="spikelet at early flowering"
/dev_stage="Feekes' scale 6"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid clones in the TJ Clone lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 146 a 196 c 156 g 134 t

ORIGIN

Query Match 17.0%; Score 396; DB 13; Length 632;
Best Local Similarity 82.0%; Pred. No. 3.4e-73;
Matches 456; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1362 GTGCTTTGTAATCCCGCTGTCTTTCGAACTTAACAAAGAGCACCAGATGAA 1421
DB 1 GCTGCTTTCGTCTCCGCTCTCGTTTATCCAACTCTGACAAAGAGCAGGAGCTTGA 60
QY 1422 AAAATAAAGCTGAGACGACCAAGTCTAATATGTTGGCTGGCTGATGAGAGAGCTGTG 1481
DB 61 AAAATAAAGCTGAGAGCAGCAATCGTAATATGTTGGCTGGCTGATGAGAGAGCTGTG 120
QY 1482 TCGATTGCTTTCGTTTACAATAAGTTTACAAGATCTGGCCATCTCAGTGCACGGCAAT 1541
DB 121 TCGATCGCTTTCGTTTACAATAAGTTTACAAGATCTGGCCACACACAGCTACACGGCAAC 180
QY 1542 GCAATAATGATCACAGACCAATCATCTGTCTTCTTTTAGCACTATGTTATTTGGGATG 1601
DB 181 GCGATAATGATCACAGCACCACATCTGTCTTCTTTTAGCACTATGTTATTTGGCATC 240
QY 1602 ATGACAAAGCCATTGATCAGGCTGTCTACCGGCTCAGGCGCTCTGTCTACCTCTGAG 1661
DB 241 TTGACAAAGCCCTCTGATCCGGTCTCTGCTGCCCGGTGAGCAACGGCCGCCCTCGGAC 300
QY 1662 CTTTCATACCAAGTCCCTGCAATCTCTCTCTTCAAGCATGCAAGGTTCTGACCTC 1721
DB 301 CCGCGTCAACCGAGTCTCTGCACTCTCTCTCTTCTTCAAGCCAGCTAGGCTCGGACCTG 360
QY 1722 GAGAGTACCAACCAATTTGTAGGCTTTCAGCTTCGGATGCTCTTCAACAGCGGAC 1781
DB 361 GAGGCGCTCTCTCCCATCTGAGGCGCTTCCAGCTCTCGGATGCTCATCAACAGCGGAC 420
QY 1782 CACACTGTCCACTACTACTGCGCGCAAGTTTCGACGCGGCTGATGGCCGATGTTTGGC 1841
DB 421 CACACATCCACTACTACTTGGCGCAAGTTTTCGACGCGGCTGATGGCCGATGTTTGGT 480
QY 1842 GGGCGGGGTTGTCGCTCTTCTCCCTTGGATCAACCAACGAGCAGGATCGGAGGAGAA 1901
DB 481 GGGCGGGGTTTGTGGCTTACTTCCCAGGATCACCCACCGATCCGACGTACTCTCGTGA 540
QY 1902 TGAACAGTCAAGAA 1917
|||||


```
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="OG5806"
/clone_lib="OG_EFGHJ lettuce serriola"
/lab_host="E.coli"
/notes=vector: pBRCDNA5f1AB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG LIB=OG_EFGHJ lettuce serriola
TAG TISSUE=flowers environmental stress
TAG SEQ=CGAATCGCGG"

BASE COUNT      175 a 134 c 146 g 278 t
ORIGIN
Query Match      15.7%; Score 366.6; DB 14; Length 733;
Best Local Similarity 70.9%; Pred. No. 5e-67;
Matches 486; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

Qy 340 CGACTCGACTACGGTGGTGTGTCATCAACCTGTCGTCGCGCTCTCTGCGCCT 399
Db 47 CTAGCTCTGAGTACTCTTCCATTGCTCTATGAATCTGTTGTTGCTCTCTTTGCTT 106
Qy 400 GCATCGCTCCGGCCACTCTCTCAGAGAGATCGCTGGTCAATGAGTCCATCACCGCG 459
Db 107 GTATCGTAATCGGTATCTTTTGAAGAGAAATCGATGATGAAGAAATCATCTGCC 166
Qy 460 TCATCATCGGCTCTGCACCGCGTGTGATCTTCTGATGACCAAGGAAAGAGTCTGC 519
Db 167 TTGTCATGGTATTTGCACTGGAGTGTATTTGTTAAGCAGTGGAGAAATTCAC 226
Qy 520 ACTTATGCTCTCAGTGAGGATCTTTCTTCATCTACCTCCCTCCGATCATCTTCA 579
Db 227 ATCTTCTAGTCTCAGTGAAGATCTTTCTTCAATTTATCTTCTCCACCTATCATCTCA 286
Qy 580 ATGAGGTTTTCAGTTAAGAAAGCAATCTTCCGGAATTTTCATGACCATCATAT 639
Db 287 ATGCTGGGTTTCAGGTTAAGAAAGCAATTTTTCGCAATTTTCATGACCATTTGCTAT 346
Qy 640 TTGAGCGCTCGGCAATGATATCTTTTTCACAAATATCTATGCTGCCAATTCGAATAT 699
Db 347 TTGGTGTCTTTGGCACTGTGATATCTTTCACCATCATATCATTTGGTGTCTATAATTT 406
Qy 700 TCAGCAGAAATGAACATTTGGAACGCTGGATGATGAGAGATTTCTTTCGCAATTTGGAGCCATCT 759
Db 407 TCCAAAGGATGGATGTTGGTACCTTGGAGCTTGGAGACTTCTTTCGCAATTTGGTGAATAT 466
Qy 760 TTTCTGACAGATCTGCTGACATTCGAGTCTCCTCAATCAGGATGAGACACCTTTT 819
Db 467 TTTGAGCACCAGATTCGGTTTGCATTTGCAAGTGTGAAATCAGGATCAGACACCTTTAT 526
Qy 820 TGTACAGTCTGGTATTCGGTGAAGTGTGTGGAACGATGCTTACATCAATTTGCTTTTCA 879
Db 527 TATATAGTTTGGTGTGGTGAAGTGTGGTGAATGATGACCATCATGTTGTCATCTTCA 586
Qy 880 ACGCACTACAGAACTTTGATCTTTGCCATAGATGCGGCTGTCTGTTCTGAAATTTCTGG 939
Db 587 ATGCAAGTCAAAACTTTTGATCTCTCAATCACAATCAGTCTGTTGCAATTTCAACTGATG 646
Qy 940 GGAATCTTTTATTTATTTTGTGCGACACCTTCTTGGAGTATTTGCTGGATGCTCA 999
Db 647 GAAATTTCTTTTATTTATTCATCAACAGCACACTTCTAGGAGCTGGAGCTGGGCTACTAA 706
Qy 1000 GTGCATACATAATCAAGAGCTATA 1024
Db 707 GTGCTTATATTAAGAGCTATA 731
```

RESULT 11
BQ612167
LOCUS

DEFINITION BQ612167 607 bp mRNA linear EST 26-JUN-2002
sap80d01.v1 Gm-cl087 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl087-7057 5', similar to TR:Q9SS27 Q9SS27 PUTATIVE SODIUM PROTON
EXCHANGER. ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BQ612167
BQ612167.1 GI:21601836
EST.
soybean.
Glycine max

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 607)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R., and Wilson, R.

TITLE
JOURNAL
COMMENT

Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: cu@resgen.com web site:
www.resgen.com

FEATURES

Seq primer: -40RP from Gibco
High quality sequence stop: 479.

source

1. 607
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl087-7057"
/clone_lib="Gm-cl087"
/tissue_type="Roots"
/lab_host="DH10B"
/note="vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The mRNA was prepared using polyattract mRNA system
from PROMEGA. The cDNA was prepared using the STRATAGENE
kit. Complementary DNA was synthesized from mRNA using a
primer consisting of a poly(dT) sequence with a XhoI
restriction site
(5'GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTTTT).
EcoRI adapters (5'-OH-AATTCGACGAG and 3'-GCCGTGCTCp) were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction sites of the pBluescript
vector. The vector was previously dephosphorylated. The
ligated cDNA fragments were transformed into DH10B by
electroporation. Library is in LB medium with ampicillin
and glycerol 8%. Average insert size: 800 bp."

BASE COUNT

141 a 118 c 133 g 215 t

ORIGIN

Query Match 15.6%; Score 362.8; DB 14; Length 607;
Best Local Similarity 76.5%; Pred. No. 3.4e-66;
Matches 445; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

Qy

803 GGATGAGACACCTTTTGTACAGTCTGGTATTCGGTGAAGGTGTGTGAACGATCTAC 862

Db

25 GGATGAGACACCTTTGCTGACAGTCTGTTTGGGAGGGTGTGTGAATGATGCTAC 84

Qy

863 ATCAATTGTCTTTTCAACGCACTACAGAACTTTGATCTTGTCCACATAGATCGGCTGT 922

Db 85 ATCAGTGGTCTTTTCAATGCAATCAAGAGCTTTCACCTCAACCAAAATGACTCTTCAAT 144

Qy 923 CCGTCTGAAATCTTTGGGAACTCTTTTATTTATTTTGTGAGACACCTCTCTTGGAGT 982

Db 145 TGCTGTACATTTTGGGAAATTTCTTGATCTATTTATGCAAGACACATGCTTGGAGT 204

Qy 983 ATTTCTGGAATGCTCAGTGCATACATCAATCAAGAGCTATACATTTGGAAGCAATTTCTAC 1042

Db 205 TTTGACAGGCTCTACTAGTCTTACATTTAAAAAGCTGTACATTTGGCAGGCACTCTAC 264

Qy 1043 TGACGCTGAGTTGGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTGGCTGAGTT 1102

Db 265 AGATCGTGAGGTTGCTCTATGATGTTAATGGCATACCTGCTCTACATGCTTGGCTGAAT 324

Qy 1103 GCTAGATTGAGCGGCAATCTCACGCTATTCTCTGTGTATTTGTAATGTCACATTTACAC 1162

Db 325 ATGTTATCTGAGTGCAATCTCACGCTATTCTCTGTGTATTTGTAATGTTATGTTCTCATTTATAC 384

Qy 1163 TTGGCAATACGTCACAGAGGTTCAAGAGTTTACAACAAGACAGCAATTTGCAACTCTGTC 1222

Db 385 CTGGCAATACGTCACAGAGGTTCAAGAGTTTACAACAAGCACTTCTTTTGCAACCTTGTG 444

Qy 1223 CTTCAATGCTGAGCTTTCTCTCTGATGTTGGGATGATGATGATTTGGAATTTGAAAA 1282

Db 445 ATTTGTTGCTGAGATCTTTATCTCTCTTATGTTGGTATGGAATGCTTTGGACATTTGAAAA 504

Qy 1283 ATGGAGTTTGGCAGTGACAGACCTGGCAATCCATTTGGGATGATGATTTTCTAGG 1342

Db 505 ATGGAATTCGTCAGTGATAGCCCTGGGACATCTGTAGCAACTAGTGAGTATTTGGG 564

Qy 1343 ATTTGTTCTGATTTGAAGAGCTGCTTTTGTATTTCCCGCTGTC 1384

Db 565 TCTAATCTCTTGGAGAGCAGCTTTTGTATTTCCCGCTATC 606

RESULT 12

BQ163913 666 bp mRNA linear EST 24-APR-2002

LOCUS 952081B08.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea

DEFINITION mays cDNA, mRNA sequence.

ACCESSION BQ163913

VERSION BQ163913.1 GI:20300970

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 666)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952081 row: B column: 08.

Location/Qualifiers

1. .666

/organism="Zea mays"

/cultivar="BMS (Black Mexican Sweet)"

/db_xref="taxon:4577"

/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"

/tissue type="suspension culture"

/dev stage="mixed logarithmic and stationary growth phases"

/lab_host="DH10B"

/note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The

library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT 149 a 155 c 153 g 209 t

ORIGIN

Query Match 15.5%; Score 361; DB 14; Length 666;

Best Local Similarity 71.4%; Pred. No. 7.8e-66;

Matches 475; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 444 GAGTCCATCACCGGCTCATCATCGGCTCTGCACCGCGGTGGTATCTTGTGTATGACC 503

Db 2 GAGTCCATCACCGGCTCTTTCATCGGCTGGGAACTGGAGCGGTATCTCTGTCGCTCG 61

Qy 504 AAAGGAGAGCTCGCACTTATTCGTCTTCAGTGAGGATCTCTTCTTCATCTACCTCTC 563

Db 62 AGCGGGAAGCAATTCGCGGTGCTGTTTACGAGGAGACCTCTCTTTATTTACCTGTG 121

Qy 564 CTTCCGATCATCTTCAATGCAAGTCTTTCAGGTAAGAAAAAGCAATCTTCGGGAATTC 623

Db 122 CCGCGATCATATTCAATGCAAGGTTCCAACTGAAGAAGAACAGTCTTTTGGAACTTC 181

Qy 624 ATGAGATCAATTTATTTGGAGCGCTGGGACAATGATATCTCTTTTCAATATCTATT 683

Db 182 ATTACTATTACACTGTTTGTGTGCACTTGGCACTTGTATCTCTTTTACTGTATATCCCT 241

Qy 684 GCTGCCATTGCAATATTTCAGCAGAAATGAACATTGGAACGCTGGATGTAGGAGATTTCT 743

Db 242 GCGCTCTAGACTTAATTAAGGCTTAATATCGCGCACTTGAACCTGGAGACTATCTT 301

Qy 744 GCAATTGGAGCCATCTTTTCTGCGACAGATTTCTGTGCAATTCGAGGTCCTCAATCAG 803

Db 302 GCACCTTGGGGCAATATTCTCGGCCACAGACTCGGTTTGACCTTGCAGGTGTAAAGCAA 361

Qy 804 GATGAGACACCTTTTGTACAGTCTGATATTCGTTGAAGTGTGTGAAAGATGCTACA 863

Db 362 GATGAGACACCAATCTTTGTACAGCTCTGTGTTGTTGAAGGTGTGTCAATGACGCACT 421

Qy 864 TCAATTGTCCTTTTCAAGCACTACAGAACTTTTCATCTTGTCCACATAGATGCGGCTGTC 923

Db 422 TCTGTTGTTGTTTCAATGCAATCCAGAACTTTGATCTCGGAAATATCAGAGTGCCAAA 481

Qy 924 GTTCTGAAATTTCTGGGGAATCTTTTATTTATTTTGTGCGAGCACCTTCTCTTGGAGTA 983

Db 482 TTACTGAACTTCATGGCAGTTTCTTTATCTGTTCTGCTCCAGCACCAATCTTGGAGTA 541

Qy 984 TTTGCTGATTTGCTCAGTGATATCAATTAAGAAGCTATACATTTGAAGCACTTCTACT 1043

Db 542 GCTTCTGGACTTCTTAGTGTCTTATACCAATTAAGAAGTTGTACTTCGGCAGCAATTCACC 601

Qy 1044 GACCGTGAGTTGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTGCTGAGTTG 1103

Db 602 GATCGTGAAGTTTCCATTATGATGCTTAATGCTTATTTATCTTACATGCTAGCTGAATTG 661

Qy 1104 CTAGA 1108

Db 662 CTCGA 666

RESULT 13

LOCUS BQ317459

DEFINITION

ACCESSION BQ317459

VERSION BQ317459.1

KEYWORDS

BQ317459 638 bp mRNA linear EST 09-APR-2002

BQ317459 Y. Ogihara unpublished cDNA library, wh_yf Triticum aestivum cDNA clone whyf28e02 5', mRNA sequence.

GI:20122274

EST.

QY 1264 ATGCATTGGATATGAAAAATGGAGTTTGCAGTGACAGACCTGGCAATCCATTGGGA 1323
 Db 182 ATGCTTTGGATATCGAAGCTGGAATTTTGTGTCAGAGGCTGGATATCAATTTCCG 241
 QY 1324 TAAGCTCAATTTTGTAGGATTTGGTCTGATGGAGAGCTGTTTGTATTTCCGCTGT 1383
 Db 242 TGAGTTCAATTAATGATGGGATTAATCTGTCTGGGGAGAGCTGCTTTGTGTTTCCATTAT 301
 QY 1384 CGTTCTTGTCGAACCTAAACAAAGGACCCGAATGAAAAATAAATCACTGGAGACGCAAG 1443
 Db 302 CATCTCTCAACTTAATGAGAAATCTCGGAGCAAAAAATTAATCTTTAGGACGCAAG 361
 QY 1444 TTGTAATATGGTGGCTGGCTGATGAGAGAGCTGTGTGATTTGCTTTGCTTACAATA 1503
 Db 362 TGATAATATGGTGGCAGGTTTGTATGAGAGGCGCAGTGTCCATGGCAGTGCATATAATA 421
 QY 1504 AGTTTACAGATCTGCCATCTACTCAGCTGACGGCAATGCAATATGATCACCAGACCA 1563
 Db 422 AGTTTACTCGTGGGGACACACTCAACTGCAGGACAATGCAATATGATTACCAGCACA 481
 QY 1564 TCACTGTGCTTTCTTTTAGCACTATGATTTTGGGATGATGACAAAGCCATTGATCAGGC 1623
 Db 482 TAACCATTTGTTTATTCAGCACAAATGATTCGTTTAAATGACAAAACCCCTTATAAGTC 541
 QY 1624 TGCTGTAC 1633
 Db 542 TCCTGCTGCC 551

RESULT 15

C91832 378 bp mRNA linear EST 04-APR-2002
 LOCUS C91832 Rice panicle shorter than 3cm Oryza sativa (japonica
 DEFINITION cultivar-group) cDNA clone E31686_1A, mRNA sequence.
 ACCESSION C91832
 VERSION C91832.1 GI:3061200
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group).
 ORGANISM Oryza sativa (japonica cultivar-group).
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 378)
 AUTHORS Sasaki, T. and Yamamoto, K.
 TITLE Rice cDNA from panicle
 JOURNAL Unpublished (1997)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 PROJECT = 'RGP'
 POLYA=No.

FEATURES

Location/Qualifiers
 1..378
 /organism="Oryza sativa (japonica cultivar-group)"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="E31686_1A"
 /clone_lib="Rice panicle shorter than 3cm"
 /dev_stage="shorter than 3cm"
 /note="Organ: panicle"
 BASE COUNT 88 a 74 c 89 g 121 t 6 others
 ORIGIN

Query Match 14.6%; Score 340.4; DB 14; Length 378;
 Best Local Similarity 95.0%; Pred. No. 2.1e-61;
 Matches 359; Conservative 0; Mismatches 17; Indels 2; Gaps 1;
 QY 1013 CAAGAAGCTATACATTGGAGGCAATCTACTGACCGTAGGTTGCCCTTATGATGCTCAT 1072
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 CAAGAAGCTATACATTGGAGGCAATCTACTGACCGTAGGTTGCCCTTATGATGCTCAT 60
 QY 1073 GGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCATTTCTCACCGTATT 1132
 Db 61 GGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCATTTCTCACCGTATT 120
 QY 1133 CTTCTGTGGTATTGTAATGTACATTACACTTGGCATAAAGCTACAGAGAGTTTCAAGAGT 1192
 Db 121 CTTCTGTGGTATTGTAATGTACATTACACTTGGCATAAAGCTACAGAGAGTTTCAAGAGT 180
 QY 1193 TACAACAAAGCAGCAATTTGCAACTCTGTCTCTTCACTTGTGAGACTTTTCTTCTCTGTA 1252
 Db 181 TACAACAAAGCAGCAATTTGCAACTCTGTCTCTTCACTTGTGAGACTTTTCTTCTCTGTA 240
 QY 1253 TGTGTGGATGATGATGATGATTTGAAAATGGAGTTTGCAGTGACAGACTGGCAA 1312
 Db 241 TGTGTGGATGATGATGATGATTTGAAAATGGAGTTTGCAGTGACAGACTGGCAA 300
 QY 1313 ATCCATTGGGATAAGCTCAATTTTGTCTAGG--ATTGGTTCTGATTGGAAGAGCTGCTTTT 1370
 Db 301 ATCCATTGGGATAAGCTCAATTTTGTCTAGG--ATTGGTTCTGATTGGAAGAGCTGCTTTT 1370
 QY 1371 GTATTCCTGCTGCTGCTTC 1388
 Db 361 GNAATTCCTGCTGCTGCTTC 378

Search completed: April 5, 2003, 15:54:29
 Job time : 3725 secs

